Run

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Post-processing: Minimum Match 0%
Listing first 45
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Perfect score:
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gb_gss15: *
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                                 Length DB
  675
  64
42
                                  IJ
 AL119269
AI099199
                                                                SUMMARIES
                               Description
AL119269 DKFZp761M
AI099199 ue40c07.y
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Minimum Maximum

DB DB

Searched:

Sequence:

Database

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AL119269 675 bp mRNA EST 27-SEP-1999
DKFZPF761M0513_r1 761 (synonym: hamy2) Homo sapiens cDNA clone
DKFZP761M0513 5', mRNA sequence.
AL119269
AL119269.1 GI:5925168
                       Am Klopferspitz 18a D-82152 Martinsried, Ger
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Ana
Research Center (DKFZ); Email s.wiemann@dkf.
                                                                                                                                                                                                                                                                                                     Chordata; Craniata; Vertebra
Catarrhini; Hominidae; Homo
                                                                                                                                                             sequence
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AL1203000
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AAU139680
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  the cDNA sequencing
                                                                                                                                                             version
r Genome Analysis, German Cancer
.wiemann@dkfz- heidelberg.de;
.wa sequencing consortium of the
                                                                                                                                                                                                                                                       Mewes, H.W.,
                                                                                                                                                             replaced
                                                                                                                                                                                                                                                                                                                          Vertebrata;
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R59283 Y997h01.r1
AU079207 AU079207
AW047433 UI-M-BH1-AA38005 vc85b01.x
AI03002 am95907.x
AI03002 am95907.x
AI03002 am95907.x
AI120018 DKFZP761H
AI205130 an04h10.x
AI842094 UI-M-BH1-AI205130 an04h10.x
AI140019 vc85b01.y
AI390224 II-BT202-AW139646 UI-H-BI1-AA0877278 n176a05.x
AW139646 UI-H-BI1-AA08776 mn97c11.y
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AI49026 Vm87e02.r1
AI49680 Drosophil AA08776 Muj34a05.x
AA7717541 Muj26202.x
AA7717541 Muj26202.x
AA7717541 Muj26202.x
AA0717541 Muj26202.x
AA090211 Mak10c10.x
AA0890211 Mak10c10.x
AA0890211 Mak10c10.x
AA0890211 Muj26202.x
AA034745 UI-R-C2p-AA0815190 wood4c12.x
AA1018543 wu350610.x
AA137215 UI-R-C2p-AA23646 zr76h12.x
AA07689 zh23a05.x
AA15550 wu351a03.x
W15550 zb91h09.s1
AI1663371 wk32a11.y
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AI099199.
                                   AI099199 600 bp mRNA EST 20-AUG-1998 ue40c07.y1 Sugano mouse liver mlia Mus musculus cDNA clone IMAGE:1482828 5' similar to WP:T20G5.5 CE00479 CAMP DEPENDENT PROTEIN KINASE REGULATORY CHAIN + GUANINE NUCLEOTIDE RELEASING FACTORS; , mRNA sequence.
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No s1 sequence available.

This clone is available at the RZPD in Berlin.

Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6,

Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone=!bkFZp761M0513"
/clone_lib="761 (synonym: h:
/tissue_type="amygdala"
/dev_stage="adult"
/lab_host="pH108"
/note="Vector: pSport1: Sit
/note="Vector
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574

KEYWORDS SOURCE ORGANISM ACCESSION VERSION

EST.

REFERENCE

Homo sapiens
Eukaryota; Metazoa; C
Eutheria; Primates;
L (bases 1 to 675)
L (bases 1 to 675)

COMMENT

EST (Ansorge, Benes, of Unpublished (1999) On Jun 22, 1998 this secontact: Ansorge W

EMBL

TITLE JOURNAL AUTHORS

> Wiemann, S. Ansorge, W.,

Benes, V.,

RESULT AL119269 LOCUS

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  181
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                                                                                                      tgaggagettetteatattaaageettateeeatetttetaeeacagtgaaaegagagtt 1023
                                                                                                                                                                        GAGAATGATCCTGCGAAAACCACCTGGCCAGAGGACTGTGGATGACCTAGAGATTATCTA
                                                                                                                                                                                               gaggatgatccttcgcaaaccacctggccagaggactgtggatgacctagagattatcta
                    agcaggtgttctcattttttgagtctcacgccaaaggaggactgtgttgtttaaccaggg 1083
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (1996)
On Apr 18, 1995 this sequence version repl
Contact: Marra Myouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Lo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 (bases 1 to 600)
Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubu, Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylle, T., Lennon, G., Soares, B., Wilson, R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Waterston, R. The WashU-HHMI Mouse EST Project
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Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus
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house mouse
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: mouseest@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                       Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           //note="Torgan: liver; Vector: pME18S-FL3; Site_1: DraIII (CACTGTGTG); Site_2: DraIII (CACCATGTG); 1st strand cDNA was primed with an oliqo(dT) primer [ATGTGGCCTTTTTTTTTTTTTTTTTTTT], double-stranded cDNA was ligated to a DraIII adaptor [TGTTGGCCTACTGG], digested and cloned into distinct DraIII sites of the pME18S-FL3 vector (5' site CACTGTGTG, 3' site CACCATGTG). XhoI should be used to isolate the cDNA insert. Size selection was performed to exclude fragments <1.5kb. Library constructed by Dr. Sumio Sugano (University of Tokyo Institute of Medical Science). Custom primers for sequencing: 5' end primer CTTCTGCTCTAAAAGCTGCG and 3' end primer CGACCTGCAGCTCGAGCACA."
                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone="IMAGE:1482828"
/clone_lib="Sugano mouse
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92.3%;
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Pred. No. 3.2e-139;
0; Mismatches 46;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CGATGCTCCAAGAGCTGCCTCCATTGTTCTTCGGGAAGATAATTGTCACTTCCTAAGAGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AL119765 409 bp mRNA
DKFZp761D0424_r1 761 (synonym: h
DKFZp761D0424 5', mRNA sequence.
                                                                                                                                                                                                                                                                                  Am Klopferspitz 18a D-82152 Martinsried, Germany This is the 5' sequence of the clone insert Clone from S. Wiemann, Molecular Genome Analysis, German Cance Research Center (DKF2); Email s.wiemann@dkfz- heidelberg.de; sequenced by GBF within the cDNA sequencing consortium of the
                                                                                                                                                                                                                                                                                                                                                                                  Unpublished (1999)
On Jun 22, 1998 this sequence version replaced gi:3247137.
Contact: Bloecker H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AL119765.1 GI:5925664
EST.
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                  Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
                                                                                                                                                                                                                 This clone is available at the RZPD in Berlin. Please contact the RZPD: Ressourcenzentrum, Heubnerweg
                                                                                                                                                                                                                                                                      German Genome Project
                                                                                                                                                                                                                                                                                                                                                                                                                                       EST (Bloecker, et al.)
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                                                                                                                                                                                                                                                   No s1 sequence available.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (bases 1 to 409)
                 106
                 þ
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/clone_lib="761 (synonym: hamy2)"
/tissue_type="amygdala"
/dev_stage="adult"
/lab_nost="DH10B"
                                 /note="Vector:
                                                                                                                                 /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                Location/Qualifiers
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                 90 c
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                 Site_1: NotI; Site_2: SalI"
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Query Match
Best Local Similarity
Matches 405; Conserv

Conservative

0,

Score 402.6; DB 64 Pred. No. 8.1e-104; 0; Mismatches 4;

64;

409;

Indels Length

0;

Gaps

0;

13.4%;
99.0%;

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REFERENCE
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                                                                                                                                                                                       Email: est@watson.wustl.edu
Insert Size: 451
High quality sequence stops: 315 Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 451 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                    Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M. Parsons,J., Rikin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R59283 446 bp mRNA EST 24-MAY-1995
y997h01.r1 Soares infant brain lNIB Homo sapiens cDNA clone
IMAGE:41798 5' similar to SP:T20G5.5 CE00479 CAMP DEPENDENT PROTEIN
KINASE REGULATORY CHAIN + GUANINE NUCLEOTIDE RELEASING FACTORS ;,
                                                                                                                                                                                                                                                                                                                                                                     The WashU-Merck EST
Unpublished (1995)
Contact: Wilson RK
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                                                                                                                                                      High quality sequence stop:
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theria; Primates; Catarrhini; Hominidae; Homo.
(bases 1 to 446)
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                                                                                                                                                                                                                                                                                                 Forest Park Parkway,
314 286 1800
314 286 1810
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/dev_stage="73 days
                /clone_lib="Soares infant brain
/sex="female"
                                                                                    /organism="Homo sapiens"
/db_xref="GDB:414339"
                                                                                                                                       Location/Qualifiers
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cycatyattycaaatacyyccayaacaytyayatactacayyayccaacccttcaatcct 2833
                                                                                                                 acatttactcatgaggggaacaagacgttcattgacaatctagtaaactttgaaaaaatg 2773
                                                                              CGCATGATTGCAAATACGGCCAGAACAGTGAGATACTACAGGAGCCAACCCTTCAATCCT 239
                                                                                                         ACATTTACTCATGAGGGGAACAAGACGTTCATTGACAATCTAGTAAACTTTGAAAAAATG 179
                                                                                                                                                                                          411;
                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                 142
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                                                                                                                                                                                               12.9%;
98.6%;
                                                                                                                                                                                                                  Roubica
                                                                                                                                                                                         0;
                                                                                                                                                                                               Score 387.2; DB 2
Pred. No. 2.1e-99;
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ACCESSION
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                                                                                                                JOURNAL
                                                                                                                                              TITLE
                                                                                                                                                                            AUTHORS
           Eutheria; Rodentia; Sciurognathi; Muridae; h
1 (bases 1 to 541)
1 (bases 1 to 541)
Hashimoto, K., Kusuda, J., Toyoda, A., Tanuma, i
Suzuki, Y., Sasaki, M. and Sugano, S.
Isolation of full-length cDNA clones from a
library made by oligo-capping method
Unpublished (1999)
On Jun 22, 1998 this sequence version replac
Contact: Ratsuyuki Hashimoto
Division of Genetic Resources
National Institute of Infectious Diseases
23-1, Toyama 1-chome, Shinjuku-ku, Tokyo 162
Email: khashi@nih.go.jp
                                                                                                                                                                                          Mus musculus
Bukaryota; Metazoa; Chordata; Craniata; Ver
Putheria; Rodentia; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                      AU079207
AU079207
5', mRNA
                                                                                                                                                                                                                                                     house mouse
                                                                                                                                                                                                                                                                           EST.
                                                                                                                                                                                                                                                                                                         AU079207
                                                                                                                                                                                                                                                                                        AU079207.1
 http://www.nih.go
                                                                                                                                                                                                                                                                                                                      sequence.
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Sugano mouse
                                                                                                                                                                                                                                                                                                                                     brain
jp/yoken/genbank,
                                                                                                                                                                                                                                                                                                                                     mncb
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                                                                                                                                                                         Tanuma, R.,
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                                                                                                                                                                                                       Murinae;
                                                                                                                                           mouse
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                                                                                                                                                                                                       Mus.
                                                                                                                                                                                                                         Mammalia;
                                                                                                                                         CDNA
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REFERENCE
AUTHORS
TITLE
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VERSION
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AW047433/c
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Bonaldo, M.F., Lennon, G. and Soares, M.B. Normalization and subtraction: two appr discovery
                                                                                                               AW047433 411 bp mRNA EST UI-M-HH1-all-c-07-0-UI.SI NIH_BMAP_M_S2 Mus UI-M-BH1-all-c-07-0-UI 3', mRNA sequence. AW047433 1 GI:5907962
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                                                   Eukaryota; Metazoa;
Eutheria; Rodentia;
                                                                              Mus musculus
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/organism="Mus musculus"
/strain="C57BL"
/db_xref="taxon:10090"
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                                                   Chordata; Craniata; Vertebrata; Sciurognathi; Muridae; Murinae;
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Pred. No. 1.4e-86;
0; Mismatches 37;
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                                                                                                                                                                                                                                                   AGTAGCTGACAAACTGGGCTCAGGGGAAGGCCTGATAATCGTCAAGATGAACTCTGGAGG
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                                                                                                     acgcctqtttgcttgcccgcgagagcaattcgattcactgactcccttaccagaacagga 2193
                                                                                                                                                                 AGAAAAGGTGGTGCTGAAATCTAATGATGTTTCAGTATTTACGACGCTCACCATTAATGG
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Contact: Chin, H
National Institute of Mental Health
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Fax: 301 443 9890
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Seq primer: M13 Forward POLYA=Yes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: mEST@mail.nih.gov
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="vector: pr/T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; The NIH_BMAP_M_S2 library is a subtracted library derived from NIH_BMAP_M_S1, which in turn is a subtracted library derived from a mixture of normalized libraries from ten regions of the mouse brain (cerebellum, brain stems, olfactory bulbs, hypothalamus, cortex, amygdala, basal gangila, pineal gland, striatum, hipoccampus). The driver used for subtraction consisted of a pool of 5,000 clones obtained from non-normalized and normalized mouse brain contained from non-normalized and normalized mouse brain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TAG_SEQ=ACGGC"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone="UI-M-BH1-all-c-07-0-UI"
/clone_lib="NIH_BMAP_M.82"
/dev_stage="27-32 days"
/lab_host="DH10B (Life Technologies)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1998 this sequence version replaced
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 325.8; DB 6
Pred. No. 6.6e-82;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              on Sep 12, 1996 this sequence version replaced Contact: Marra M/Mouse EST Project Washington University School of MedicineP 4444 Forest Park Parkway, Box 8501, St. Louis,
                                                                                                                                                                                                                                                                                                                                                                                                             Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 (bases 1 to 361)
Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque,
Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
Theising, B., Wylle, T., Lennon, G., Soares, B., Wilson, R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AA388UU5 361 DP mRNA
VC85D01:11 KO mouse embryo 11 5dpc Mus musculus cDNA clone
IMAGE:789769 5' similar to WP:T20G5.5 CE00479 CAMP DEPENDENT
PROPER KINASE REGULATORY CHAIN + GUANNINE NUCLEOTIDE RELEASING
                                                                                                                                                                                                                                                                                                                                                                                         High
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tel: 314 286 1800
Fax: 314 286 1810
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Location/Qualifiers
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                             constructed Wang."
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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:789769"
                                                                                                                                                                                                                                  /tissue_type="embryo"
/dev_stage="11.5dpc"
/lab_host="DH10B"
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                                                                                                                                                                                                                                                                                        /clone_lib="Ko mouse embryo 11 5dpc"
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                                  by Dr. Minoru S. H. Ko and Dr. Xiaohong
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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    atgcagctcaagctaataagaaccatcaggatgtccggagttatgtacggcaattaaatg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@mage.llnl.gov) for further information.
Possible reversed clone: similarity on wrong strand
Possible reversed clone: polyT not found
Seq primer: -40mi3 fwd. Erf from Amersham
High quality sequence stop: 269.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jos Krizman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wylie, T., Waterston, R. and Wilson, R. WashU-NCI human EST Project Unpublished (1997)
On Jan 19, 1998 this sequence version replaced gi:2285771.
                                                                                                                                                                                                                                                                                                                                                                                                                                  Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. I Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AI003002 317 bp mRNA EST 09-JUN-1998 am95g07.sl Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE:1683900 3' similar to TR:Q92565 Q92565 MYELOBLAST KIAA0277.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Wilson RK
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1 (bases 1 to 317)
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/tissue_type="schizophrenic brain S-11 frontal lobe"
/dev_stage="34 years old"
                                                                 /sex="male"
                                                                               /clone="IMAGE:1683900"
/clone_lib="Stratagene schizo
                                                                                                                                           /organism="Homo sapiens"
/db_xref="taxon:9606"
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Pred. No. 6.6e-79;
0; Mismatches 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Box 8501, St. Louis,
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Matches 314; Conserv
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                                                                                    Am Klopferspitz 18a D-82152 Martinsried, Germany This is the 5' sequence of the clone insert clone from S. Wiemann, Moletular German Analysis, German Cancer Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de; sequenced by MediGenomix within the cDNA sequencing consortium the German Genome Project.
                                                                                                                                                                                                                                  Unpublished (1999)
Unpublished (1999)
On Jun 22, 1998 this sequence version replaced g1:3247395.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AL120018 343 bp mRNA ES DKFED761H222_r1 761 (synonym: hamy2) Homo DKFED761H222 5', mRNA sequence.
AL120018
This clone is available at the RZPD in Berlin. Please contact the RZPD: Ressourcenzentrum, Heubnerweg Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
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1 (bases 1 to 343)
                                                                    No s1 sequence available.
                                                                                                                                                                                                                                                                                                                                                                 Ottenwaelder, B., Obermaier, B.,
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                                                                                                                                                                                                                                                                                                                    (Ottenwaelder,
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                                                                                                                                                                                                                                                                                                                                                                   Mewes, H.W., Gassenhuber, J. and
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hes 283;
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                                                                                                                                                                                                                                                                                                                Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B., White,Y., Superson,R. and Wilson,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       an04h10.x1 Stratagene schizo brain S11 IMAGE:1684675 3', mRNA sequence.
                                                                     Email: est@watson.wustl.edu
This clone is available royalty-free through LINL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Possible reversed clone: polyT not found
Seq.primer: -40UP from Gibco
                                                                                                                                                                                                     Washington University School of Medicine
                                                                                                                                                                                                                                                            WashU-NCI human EST Project
Unpublished (1997)
On Jan 19, 1998 this sequence version
                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                 Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AI205130.1 GI:3758192
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                                                                                                                                                                   314 286 1800
314 286 1810
                                                     quality sequence stop: 240.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone_lib="761 (synonym: hamy2)"
/tissue_type="amygdala"
/dev_stage="adult"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone="DKFZp761H222"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                 Location/Qualifiers
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/organism="Homo sapiens"
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Pred. No. 4.7e-69;
0; Mismatches 4
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                                                          Contact: Chin, H
Contact: Chin, H
National Institute of Mental Health
National Institute of Mental Health
National Institute Rlvd. Room 7N-7190, MSC 9643, Bethesda, MD
                                                                                                                                                                                                                                                                                                                                                                                                                                                     AI842094 450 bp mRNA EST 14-JUL-1999 UI-M-AN1-afg-e-01-0-UI.S1 NIH_BMAP_MBG_N Mus musculus cDNA clone UI-M-AN1-afg-e-01-0-UI 3', mRNA sequence.
                                                                                                                                                   On Dec 20, 1995 this sequence version replaced
                                                                                                                                                                                              Genome Res. 6 (9),
                                                                                                                                                                              97044477
                                                                                                                                                                                                                         discovery
                                                                                                                                                                                                                                    Bonaldo,M.F., Lennon,G. and Soares,M.B. Normalization and subtraction: two approaches
                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Cranlata; Vertebrata;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
1 (bases 1 to 450)
Bonaldo, M.F., Lennon, G. and Soares, M.B.
                                                                                                                                                                                                                                                                                                                                                      Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                   AI842094.1 GI:5476307
Email: mEST@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                          house mouse.
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/dev_stage="34 years old"
/dev_stage="34 years old"
/lab_host="SOLR (kanamycin resistant)"
/lab_host="SOLR (kanamycin resistant)"
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/note="vector: Bluescript SK-; Site_1: EcoRI; Library
/note="vector: Bluescript SK-; Site_1: EcoRI; Library
/note="vector: Bluescript SK-; Shizophrenic suicide.
Sol caucasian, 50% Aleutian. Schizophrenic suicide.
Random primed into EcoRI site of ZAP II Vector. Mass
excised. Custom library. Avg insert length 1.4kb.
Material obtained by Johnston N., Torrey, E.F., Yolken R.,
and the Stanley Neuropathology Consortium - Analysis of
RNAs from the Brains of Individuals with Psychiatric
Diseases (Unpublished) Stanley Neurovirology Laboratory,
Johns Hopkins School of Medicine, Baltimore MD."
63 a 68 c 76 g 61 t
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/clone_lib="Stratagene schizo brain S11"
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'db_xref="taxon:9606"
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100.0%; Pred. No. 1.7e-65;
tive 0; Mismatches 0;
                                                                                                                                                                                              791-806 (1996)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POLYA-Yes
                              105
                                                                                                                                                                                                                                   /note-"Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; The NIH_BMAP_MBG_N library is a normalized library constructed from mouse basal ganglia. The tag is a string of 5 nucleotides present between the Not I site and the oligo-dT track. The library was constructed as described by Bonaldo, Lennon and Soares, Genome Research 6:
                       by Bonaldo, Lennon and Soares, Genome Research 6: 791-806, 1996. Tissue provided by Ms. Annie Novakovich, Zivic-Miller Laboratories.

TAG_LIB-NIH_BMAP_MBG_N
TAG_TISSUE-basal-ganglia
TAG_SED-TGTAC"

107 c 107 g 131 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone="UI-M-AN1-afg-e-01-0-UI"
/clone_lib="NHLBMAP_MBG_N"
/dev_stage="27-32 days"
/lab_host="DH10B (Life Technologies)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /strain="C57BL/6J"
/db_xref="taxon:10090"
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B δõ Вþ 20 Qy 밁 Qy 멹 밁 뫄 δÃ δõ Matches 285; Query Match Best Local Similarity 150 210 395 270 335 330 275 390 215 450 455 agaa 458 tggacaacaccccgccatgcaaccatcgttaccagggagagcagtgaactgctccgca 334 accaggatgctgtgaccatctgtaccctgggaattgggacggcctttggagagtccattc 274 CCAACTGGTATGCTGTCCTGGCTGGGTCTTTGGATGTTAAAGTGTCTGAGACCAGCAGTC 391 AGAA 147 TGGCTCCTCCCTATGGTGTTATGGAAACGGGCTCTAACAATGACAGGATTCCTGACAAGG tggctcctccttatggtattatggaaacgggctctaaccaatgacaggattcctgacaagg 454 ACCAGGATGCGGTGACCATCTGCACTCTGGGAATTGGGACAGCCTTTGGAGAGTCCATTC 331 Conservative 8.7%; 0; Score 263.2; DB 6 Pred. No. 4.9e-64; 0; Mismatches 18 DB 61; 18; Indels Length 1; Gaps 151

COMMENT

sequence contained

an oligo-dT track that was

present in the

VERSION ACCESSION

mRNA sequence. AI608196 AI608196.1 GI:4617363

RESULT 1 AI608196 LOCUS

12

DEFINITION

AI608196 277 bp mRNA EST 21-APR-1999 vc85b01.yl Ko mouse embryo 11 5dpc Mus musculus cDNA clone IMAGE:789769 5' similar to TR:Q92565 Q92565 MYELOBLAST KIAA0277. ;,

TITLE

JOURNAL

SOURCE

KEYWORDS

/ERSION

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SOURCE
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                                                                                                                                                                                   2595 tctatgcggagtttgaaagtttaatggacccttcaagggacccacagggcctacaggctga 2654
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 source
123 CATTTACTCATGAGGGGAACAAGACGTTCATTGACAATCTAGTAAACTTTGAAAAAATGC
                                                                                                                                                                                                                                              Local Sin hes 253;
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                 catttactcatgaggggaacaagacgttcattgacaatctagtaaactttgaaaaaaatgc 2774
                                                                       TCTATGCGGAGTTTGAGAGCTTGATGGATCCTTCCAGAAACCACAGGGCATACAGGCTGA 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (1999)
on Jun 22, 1998 this sequence version replaced gi:3247167.
Contact: Marra MyMashU-NCI Mouse EST Project 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Marra,M., Hillier,I., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R. Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; 1 (bases 1 to 277)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ;
IMAGE Consortium (info@image.llnl.gov) for further ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Waterston, R. and Wilson, R.
The WashU-NCI Mouse EST Project 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This read is a RESEQUENCE of a previously sequenced mouse clone This read has been verified (found to hit its original self in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus
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Seq primer: Primer n
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                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                          GRATAGTCGAGGTCAAT 3'. The cDNAs were size-selected and amplified by long-range PCR using Ex Taq polymerase for 18 cycles. The PCR-amplifiable cDNA mixture went through one round of equalization and was digested with Sall/NotI and cloned into the Sall/NotI sites of the pSPORTI plasmid vector (Life Technologies). The library was constructed by Dr. Minoru S. H. Ko and Dr. Xiaohong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /dev_stage="11.5dpc"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:789769"
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                                                                                                                                                                                                                                                                    .8; DB 48;
1.9e-57;
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οy

2388 ttcagttttgggtcgtcactgagatctgcctttgttctcagctcagcaagcgtgttcagc 2447

0; Mismatches Score 220.4; DB 4 Pred. No. 7.8e-52;

Indels Length

0

Matches 302; Query Match

Local

Similarity

7.3%;

DB 45;

441; 0;

Conservative

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REFERENCE
AUTHORS
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Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y.,
Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R.,
Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R.,
Waterston.R and wilson p
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: mouseest@watson.wustl.edu
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/tissue_type="lung"
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/dev_stage="6-8 month old"
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/note="Organ: lung; Vector: pBluescript Sk-; Site_1: lung; Vector: pBluescript Sk-; Vector: pBl
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/sex="female"
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                                                                                                                                                                                           Email: asimpsoneludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer
This sentry can be seen in the following URL
(http://www.ludwig.org.br/seq/gethtml.pl?tl=IL&t2=IL-BT202-
                                                                                                                                                                                                                                                                                              On Jun 5, 1998 this sequence version replaced contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509
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Seg primer: puc 18 forward.
Location/Qualifiers
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The FAPESP/LICR Human Cancer Genome Project
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+55-11-2707001
 /note="Organ: breast; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue
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                                                                                                               /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                         /dev_stage="Adult"
                                                                                                   /clone_lib="BT202"
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                  Unpublished (1997)
On Jul 7, 1999 this sequence version
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert Strausberg@nih.gov
                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 444)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGA
                                                                                                                                                                                                                                                                                                                                                     AW139646 444 bp mRNA
UI-H-BI1-adr-c-04-0-UI.sl NCI_CGAP_Sub3
IMAGE:2717575 3', mRNA sequence.
AW139646
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a 127 c 143 g 94 t 27 others
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/note="vector: p7735-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; The NCI_CGAP_Sub3 library is a subtracted library derived from the NCI_CGAP_Sub1 library, which is a subtracted library derived from BI. BI constitutes a mixture of 21 normalized or subtracted NCI_CGAP_P722, NCI_CGAP_P728, NCI_CGAP_CO10, NCI_CGAP_P722, NCI_CGAP_LID, NCI_CGA
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TAG_LIB=NCI_CGAP_Lu19
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                                                            gatatgacatttactcatgaggggaacaagacgttcattgacaatctagtaaactttgaa 2767
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Search completed: April 22, Job time: 9891 sec 2000, 11:27:55

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-689.422 Million cell updates/sec
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Copyright (c) 1993 - 2000 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

HSU78516 4278 bp mRNA PRI 08-JAN-1999 Homo sapiens cAMP-regulated guanine nucleotide exchange factor II (CAMP-SEFII) mRNA, complete cds. U78516 U78516.1 GI:4115908

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MEDLINE
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AUTHORS
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2 (bases 1 to 4278)
5pringett, G.M., Kawasaki, H., Graybiel, A.M.
5pringett, G.M., Kawasaki, H., Graybiel, A.M.
Springett, G.M., Graybiel, A.M.
Springett, G.M., Graybiel, A.M.
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Springett, G.M., Kawasaki, H., Graybiel, A.M.
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A familly of cAMp-binding proteins that directly activate rapl Science 282 (5397), 2275-2279 (1998)
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awasaki, H., Springett, G.M.,
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EKEHENILHOICCLGGYZENLEKGITLERQGDIGTNWYANLAGSIDVKVSETSSHODAV
TICTLGIGTAFGES ILDNTPRHATIVTRESSELLIEQKDFKALWEKYRQYMAGLLAP
PYGYMETGSNINDRIPDKENTPLIEPHYPLRPANTITKYPSEKILRAGKILWAKILGRA
PHMIRDRKYHLKTYRQCCVGTELVDWMMQOTPCVHSRTQAVGMWQVLLEDGVLNHVDQ
EHHFQDKYLFYRFLDDBHEDAPLPTEEEKKECDBELQDTWILLSQMGPDAHMMHILR
PHGQRYLFYRELLHIKALSHLGSTYVKRELAGVLIFESHAKGGTVLFNQGEBGT
SWYIILKGSVNVVIYGKGVVCTLHEGDDFGKLALVNDAFRAASIVLREDROHFLRVDK
EDFNRILRNDEANTVRLKEHDODVLVLEKVPAGNRGSDEVLFKVYCMGTPEKI
LEHFLETIRLEATINEATDSVLNDFIMMHCVFMPNTQLCPALVAHYHAQPSQGTBQEK
MDYALNNKRRVIRLVLQWAAMKGDLLQBDVSMAFLEEBYVSVSDDARMIAAKEQLP
ELEKIVKQISBDAKAPQKKHKVLLQQFNTGDERAQKRQPIRGSDEVLFKVYCMDHTYT
TIRLEATINEATDSVLNDFIMMHCVFMVTGLGCSGEKVYLKFTLTINGRL
FACPRRQFDSLTFLPERQGEFTYGTVGTGFTELMSKGLAXQWTIVAGKEFTLTINGRL
FACPRRQFDSLTFLPERQGEFTYGTVGTGFTELMSKGLAXQWTIVAGKEFTKITAHCKE
YKILMSFFALVMGLSNIAVSRLALTWEKLPSKFKKFYAFESLMDPSRHHRAYRLTVA
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/codon_start=1
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/db_xref="GI:4115909"
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/db_xref="taxon:9606"
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  TAAGAGTAGACAAGGAGGATTTCAACCGGATCCTAAGGGACGTGGAGGCGAATACAGTCA
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Direct Submission
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U78168.1
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A family of cAMP-binding proteins that directly Science 282 (5397), 2275-2279 (1998)
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Direct Submission
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Epac is a Rapl guanine-nucleotide-exchange factor direct activated by cyclic AMP
Nature 396 (6710), 474-477 (1998)
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           LLFEPHSKAGTVLFSQGDKGTSWY INKGSVNVVTHGKGLVTTLHEGDDFGQLALVND
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                                      TCAAGGAGCAGAAGCTCCAATTCCTTTTGCCGTCATGTTTGGCCTCAGCAACTCGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (14-NOV-1996) Center for Cancer Research/Department of Brain and Cognitive Sciences, Massachusetts Institute of Technology, 77 Massachusetts Avenue, E17-540, Cambridge, MA 0213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kawasaki,H., Springett,G.M., Mochizuki,N., TOKI,S., Manaya,m. Matsuda,M., Housman,D.E. and Graybiel,A.M.
A family of cAMP-binding proteins that directly activate Rapl Science 282 (5397), 2275-2279 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kawasaki, H., Housman, D.E. Direct Submission
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/transiation-"MVLKRMHRPRCCSYQLVFEHRRPSCIQGLRWTPLINSEGSLDFR
VSLEQATTEHYHKAGKLLYRHLLATYPTLIRDRYHLHRQCCSGRELVDGILALGL
GVHSRSQAVGICQVLLDEGALCHVKHDMTFQDRDAQFYRFPGPPDPAGTHDYEEELV
EAMALLSQRGPDALLTYALRKSPGQRTDEELDLIFEELVHIKAVAHLSNSYKRELAAV
LLFEBHSKAGTYLFSQGENGTSWYITNKGSVUNVTRGKGLVTTLHEGDDRGQLALVND
APRAATIILRENNCHFLREWDKQDFNRIIKOSVUNVTRGKGLVTTLHEGDDRGQLALVND
APRAATIILRENNCHFLREWDKQDFNRIIKOSVUNVTRGKGLVTTLHEGDDRGQLALVND
APRAATIILRENNCHFLREWDKQDFNRIIKOSVAHDPFETFLSDELTHHSYFMPCTQL
FAALLHHFHVEPSEPAGGSEQERSTYICNKRQQILRLVSRWALYSPMLRSDPVATSF
LQKLSDLVSRDTRLSNLLREQYVEFRRHHRLENGCGNVSPQTKARNAPVWFPNHEEPL
PSSAGAIRVGDKVPDICRPDHSVLTLHLPVTASVREWMALAHEDHWTKGQVLVKVN
SAGDVVGLQPDARGVATSLGLURRIFVVDPQEVHELTPHFEQLGFTLGSSEMLDLVSA
KDLAGQLTEHDWNLFRRIHQVELHYVLGPOHLRDVTTANLERFWRRFNRLQYWVATE
KDLAGQLTEHDWNLFRRIHQVELHYVLGPOHLRDVTTANLERFWRRFNRLQYWVATE
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/note="GEF domain shows highest similarity
family; contains cAMP binding domain"
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1. .3373
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/db_xref="GI:4079657"
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                                      tcgtcttacgagaagataactgccatttcttaagagtagacaaggaggatttcaaccgga
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WFEKMRMARAVBMLHHGRSHSTAPLSPURSRVSHIHEDSQASRISTCSEQSLSTRSP
ASTWAYVQQLKVIDNORELISRLSRELEP"
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ALFHOFSLKENWLOHRGTVTETEEIFCHYYITEHSYVSYKKVSSIAGEILKVVAEKI
OYAEEDLALVAITFSGEKHELOPNDLVISKSLEASGRIYVYRKOLADTLUPFARNEES
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/db_xref="GI:1665819"
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Pred. No. 2.1e-100;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 59255)
Birren,B., Linton,L., Nusbaum,C. and Lander,E.
Homo sapiens, clone RP11-22F10
Unpublished
                                                                                                                             Homo sapiens clone RP1
AC016789
AC016789.1 GI:6538791
HTG; HTGS_PHASE0.
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                                                                                                Homo sapiens
                                                                                                                                                                        59255 bp DNA
s clone RP11-22F10, LOW-PASS
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EBNCE 2 (bases 1 to 59355)

Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M., Baldwin, J., Barna, N., Beckerly, R., Boguslavkly, L., Boukhgalter, B., Brown, A., Castle, A., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Donlino, M., Donelan, L., Doyle, M., Ferreira, P., Fitzhugh, W., Forrest, C., Funke, R., Gage, D., Galagan, J., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L., Howland, J.C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., McBurla, J., Lieu, C., Locke, K., Macdonald, P., Marquis, N., McEwan, P., McGurk, A., McKernan, K., McLaughlin, J., Meldrim, J., Morrow, J., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P., Peterson, K., Pollara, V., Riley, R., Roy, A., Santos, R., Severy, P., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Tirrell, A., Vassiliev, H., Vo, A., Wheeler, J., Wu, X., Wyman, D., Ye, W.J., Zimmer, A. and Zody, M.

LE Direct Submission

Submitted (05-DEC-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA All repeats were identified using RepeatMasker:

Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html

Center code: WIBR

Center code: WIBR

Center code: Wibr project information

Center project name: 14108

Center clone name: 22_F_10

* NOTE: This record contains 76 individual
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NOTE: This record contains 76 individual sequencing reads that have not been assembled into contigs. Runs of N are used to separate the reads and the order in which they appear is completely arbitrary. Low-pass sequence sampling is useful for identifying clones that may be gene-rich and allows overlap relationships among clones to be deduced. However, it should not be assumed that this clone will be sequenced to completion. In the event that the record is updated, the accession number will 10817 preserved. 10033 9263 8485 6909 6158 7693 5395 4640 3842 3048 2285 1540 755 3841: 6157: 4639: 3047: 7692: 1539: 754: contig of 754 bp in length gap of contig gap of contig gap of gap of contig unknown le g of 775 bp unknown le unknown length of 778 bp in length unknown lengt of 763 bp in unknown lengt of 755 bp in unknown length of 794 bp in length unknown length of 770 bp in length unknown length of 792 bp in length unknown length of 784 bp in length unknown length of 751 bp in length unknown length of 798 bp in length of 785 bp unknown of 784 bp in length unknown length of 763 bp in unknown of 745 bp in unknown length of 785 bp in unknown length length

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VERSION AC014497.1 GI:0436838 KEYWORDS HTG: HTGS_PHASE2. SOURCE fruit fly. ORGANISM Drosophila melanogaster	9 AC014497 ION Drosophila pieces. ON AC014497	Qy 3009 a 3009 Db 46135 A 46135	65 – da	Qy 2889 taaatgtgattgacaaccagagaaactttatcacagatgtcacacagattagagcctcgtc 2948	Qy 2829 atcctgatgcagctcaagctaataagaaccatcaggatgtccgggagttatgtacggcaat 2888	Query Match 5.8%; Score 176.2; DB 44; Length 59255; Best Local Similarity 98.3%; Pred. No. 1.3e-38; Matches 178; Conservative 0; Mismatches 3; Indels 0; Gaps 0;	56091 56878: contig of 788 bp in gap of unknown length	e fi e	gap of unknown length 53729 54498: contig of 770 bp in gap of unknown length	unknown lengt of 780 bp in unknown lengt of 792 hp in	* 50604 513/6: config of 7/3 bp in length * 51377 52156: config of 780 bp in length	gap of unknown lengt 50603: contig of 793 bp in gap of unknown lengt	£ 5 £	gap of unknown lengt 48254: contig of 770 bp in gap of unknown lengt	of E of	gap of unknown lengt 45923: contig of 785 bp in gap of unknown lengt		43548: contig of 776 bp in gap of unknown lengt	* 41989 42772: contig of 784 bp in length * are of unknown length	* 41211 41988; contig of 778 bp in length


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REFERENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         38547 GGCGGTGTCCAGGCTGCAACAGACCTGGGAAAAGATTCCGTCGAAGTTCAGGAAGATCTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CGCCCATGAGGGCAACAAGACCAGCCTGGACGGCCTGGTGAACTTCGAGAAGATGCACAT
           Celniker, S.E., Agbayani, A., Arcaina, T.T., Baxter, E., Blazej, Butenboff, C., Champe, M., Chavez, C., Chew, M., Clesiolka, L., Doyle, C.M., Farfan, D.E., Galle, R., George, R.A., Harris, N.I., Hoskins, R.A., Houston, K.A., Hummasti, S.R., Karra, K., Kearney Kim, E., Lee, B., Lewis, S., Li, P., Lomotan, M.A., Mazda, P., Moshrefi, A.R., Moshrefi, M., Nixon, K., Pacleb, J.M., Park, S.,
                                                                                                                                                                                                                                                                                                                                                           Drosophila melanogaster chromosome 2 clone BACR04F03 (D622) RI 04.F.3 map 42D-42E strain y; cn bw sp, *** SEQUENCING IN PROGRESS, 79 unordered ricese
                                                                                                                                              Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 111455)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This sequence was identified as CDM:10210380 by the submit For further information on this sequence e-mail to fly@cel * NOTE: This is a 'working draft' sequence.

* This sequence will be replaced

* by the finished sequence as soon as it is available and

* the accession number will be preserved.
                                                                                                                                                                                                                                          Drosophila melanogaster
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1 (bases 1 to 87767)
Pfeiffer,B., Poon,L.,
                                                                                                                                                                                                                                                                  fruit fly
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/db_xref="taxon:7227"
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Sequeira, A.,
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Pred. No. 7.9e-29;
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Sethi, H., Snir, E.,
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to fly@celera.com
                                                                                                                            Blazej, R.G
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                                                           Kearney, L.,
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AL Submitted (13-MAY-1999) Drosophila Genome Center, Lawrence Berkeley, Laboratory, MS 64-121, Berkeley, CA 94720, USA
On Aug 2, 1999 this sequence version replaced gi:5629947.
For further information about this sequence, including its location and relationship to other sequences, please visit our sequence archive Web site (http://www.fruitily.org/sequence/) or send email to bdgp@fruitfly.berkeley.edu. All contigs in this submission meet the following cutoffs: length >= 200 bases.
* NOTE: This is a 'working draft' sequence. It currently consists of 79 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence as soon as it is available and the accession number will
* be preserved.
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8: contig of 906 bp in length
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                                                                         AC007624 189668 bp DNA
Drosophila melanogaster chromosome
10.F.15 map 42E-43A strain y; cn bw
***, 54 unordered pieces.
AC007624.4 GI:5670596
HTG; HTGS_PHASE1.
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36860: 36940: 38203:

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (21-MAY-1999) Drosophila Genome Center, Lawrence Berk Laboratory, MS 64-121, Berkeley, CA 94720, USA On Aug 2, 1999 this sequence version replaced gi:4887256. For further information about this sequence, including its loca and relationship to other sequences, please visit our sequence archive Web site (http://www.fruiffly.org/sequence/) or send em to bdgp@fruitfly.berkeley.edu. All contigs in this submission m the following cutoffs: length >= 200 bases.

* NOTE: This is a 'working draft' sequence. It currently consists of 54 contigs. The true order of the pieces is not known and their order in this sequence record is
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82418: contig of MRN

682491

82498: gap of unknown

1610321: contig of 23

116113695: gap of unknown

1616863: contig of 35166

4168943: gap of unknown

169169: contig of 734 bp in

170063: gap of unknown length

189169: contig of 694 bp in

189169: gap of unknown length

189169: gap of unknown length

189169: contig of 770 bp in len

189169: contig of 707 bp in len
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Blazej, R.G.,

Kearney, L.,

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FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 206;
                                Celniker, S.E., Agbayani, A., Arcaina, T.T., Baxter, E., Blazej, R.G., Butenhoff, C., Champe, M., Chavez, C., Chew, M., Ciesiolka, L., Boyle, C.M., Farfan, D.E., Galle, R., George, R.A., Harris, N.L., Hoskins, R.A., Houston, K.A., Hummasti, S.R., Karra, K., Kearney, L., Kim, E., Lee, B., Lewis, S., Li, P., Lomotan, M.A., Mazda, P., Moshrefi, A.R., Moshrefi, M., Nixon, K., Pacleb, J.M., Park, S., Pfeiffer, B., Poon, L., Sequeira, A., Sethi, H., Snir, E.,
                                                                                                                                                                                 Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                      AC008340 125681 bp DNA HTG 06-AUG-1999
Drosophila melanogaster chromosome 2 clone BACR07J20 (D918) RPCI-98
D7.J.20 map 42D-42E strain y; cn bw sp, *** SEQUENCING IN PROGRESS
                    Svirskas, R.R., Wan, K.H.,
                                                                                                                                                                                                                                                                              fruit fly.
                                                                                                                                                                                                                                                                                              HTG; HTGS_PHASE1.
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4 41017 c 40764 g 52607 t 4241 others
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/clone_lib="RPCI-98 (Roswell Park Cancer Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /map="42E-43A"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Drosophila melanogaster"
/strain="y; cn bw sp"
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Pred. No. 9.2e-29;
0; Mismatches 107;
                    Weinburg, T., Zhang, R.,
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                    Zieran, L.L. and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (02-AUG-1999) Drosophila Genome Center, Lawrence Berkeley Laboratory, MS 64-121, Berkeley, CA 94720, USA On Aug 4, 1999 this sequence version replaced 91:5670395. For further information about this sequence, including its location and relationship to other sequences, please visit our sequence archive Web site (http://www.fruitfly.org/sequence/) or send email to bdgp@fruitfly.berkeley.edu. All contigs in this submission meet the following cutoffs: length >= 200 bases.

* NOTE: This is a 'working draft' sequence. It currently consists of 92 contigs. The true order of the pieces

* is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Celniker,S.E., Agbayani,A., Arcaina,T.T., Baxter,E., Blazej Butenhoff,C., Champe,M., Chavez,C., Chew,M., Clesiolka,L., Doyle,C.M., Farfan,D.E., Galle,R., George,R.A., Harris,N.L., Hoskins,R.A., Houston,K.A., Hummasti,S.R., Karra,K., Kearne
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               * arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown
* This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kim,E., Lee,B., Lewis,S., Li,P., Lomotan,M.A., Mazda,P.,
Moshrefi,A.R., Moshrefi,M., Nixon,K., Pacleb,J.M., Park,S.,
Pfeiffer,B., Poon,L., Sequeira,A., Sethi,H., Snir,E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished
2 (bases 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rubin, G.M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequencing of Drosophila melanogaster
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g of 1134 bp in length
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                    Homo sapiens clone RP1
AC016789
AC016789.1 GI:6538791
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gap of contig

49097: 49177: 50979: 51059: 52018: 52098:

54238: 54318: 55819:

35907 35987 37437 37517 39103 39103 40010 40090 41698 41778 42479 42559

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gap o gap of

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60390: 63037: 63117: 65910: 675980: 67588: 67668: 67668: 72203: 72203:

unknown
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of 1320
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of 3135

gap of contig gap of contig

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of 4063

gap of contig gap of contig

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Center: Whitelead Institute/ MIT Center for Genome Research Center code: WIBK Web Site: http://www-seq.wi.mit.edu Contact: sequence_submissions/genome.wi.mit.edu Center project name: 14108 Center clone name: 22_F_10 **NOTE: This record contains 76 individual sequencing reads that have not been assembled into contigs. Runs of N are used to separate the reads and the order in which they appear is completely arbitrary. Low-pass sequence sampling is useful for identifying clones that may be gene-rich and allows overlap relationships among clones to be deduced. However, it should not be assumed that this clone will be sequenced to completion. In the event that the record is updated, the accession number will be preserved. 755 1539 contig of 754 bp in length gap of unknown length 1040 2284 contig of 755 bp in length gap of unknown length 2841 contig of 794 bp in length gap of unknown length 4640 5394 contig of 794 bp in length gap of unknown length 5158 6908 contig of 755 bp in length gap of unknown length 6158 6908 contig of 755 bp in length gap of unknown length 6158 6908 contig of 755 bp in length gap of unknown length 6158 6908 contig of 755 bp in length gap of unknown length 6158 6908 contig of 755 bp in length gap of unknown length 6158 6908 contig of 758 bp in length gap of unknown length 6158 6908 contig of 758 bp in length 6158 6908 contig of 759 bp in length 6159 6908 contig of 7598 bp in length 6150 6908 conti	DeArellano, K., Dewar, K., Domino, M., , FitzHugh, W., Forrest, C., Funke, R. , Gardyna, S., Grant, G., Hagos, B., He C., Johnson, R., Jones, C., Kann, L., K , Lieu, C., Locke, K., Macdonald, P., McGurk, A., McKernan, K., McLaughlin, Naylor, J., Norman, C.H., O'Connor, T, Pollara, V., Riley, R., Roy, A., San mann, N., Stojanovic, N., Subramanian, , Tirrell, A., Vassiliev, H., Vo, A., W Ye, W. J., Zimmer, A. and Zody, M. mission (05-DEC-1999) Whitehead Institute/MI (05-DEC-1999) Whitehead Institute/MI 320 Charles Street, Cambridge, MA 02 s were identified using RepeatMasker A. & Green, P. (1996-1997) Genome washington.edu/RM/RepeatMasker A. & Green, P. (1996-1997)	<pre>1 (bases 1 to 59255) 1 (bases 1 to 59255) Birren,B., Linton,L., Nusbaum,C. and Lander,E. Homo sapiens, clone RP11-22F10 Unpublished 2 (bases 1 to 59255) Birren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,M., Baldwin,J., Barna,N., Beckerly,R., Boguslavkiy,L., Boukhgalter,B., Brown,A., Castle,A., Colangelo,M., Collins,S., Collymore,A.,</pre>
20981 21755 22515 22515 23303 24107 24875 24875 25639 26380 27955 27955 28729 29508 30300 31101 32637 33421 34974 35764 36548 37312 38895	* 13940 * 14735 * 15511 * 16285 * 17071 * 17844 * 18623 * 19408 * 20210	* 10817 * 11602 * 12377 * 13154
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AC005285 209071 bp DNA INV 15-JUL-1998 Drosophila melanogaster DNA sequence (P1s DS00121 (D128), DS054 (D270), and DS00108 (D120)), complete sequence. AC005285 AC004272 AC002637 AC002638 AC003139 AC003717 AC003718 AC003140 AC003141 AC003719 AC002639 AC003142 AC003720 AC003143 AC004268 AC004269 AC002586 AC002586 AC003143 AC004568 AC004269 AC002586 AC003143 AC003131 AC003709 AC002585.1 GI:3320127
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gap of unknown length
0: contig of 794 bp in length
can of unknown length
can of unknown length
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ig of 770 bp in length
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Best Local Similarity
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                                                                                                                                                                                                                     2452 aaaaaaatttattaagatagcagcccactgtaaggagtataaaaatctgaattccttttt 2511
2572 actgccaagcaagttcaagaagttctatgcggagtttgaaagtttaatggacccttcaag 2631
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                                                                                              tgccatcgtcatgggactaagtaacattgctgtgagccgcttggcactaacgtgggagaa 2571
                                                                                                                                                                                                                                                                                                                                                                                                                                 241;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     For further information about this sequence, including its location and relationship to other sequences, please visit our sequence archive Web site (http://fruitfly.berkeley.edu/sequence/) or send email to drosophila@nhgc.lbl.gov.
Library locations: 25-2, 137-57, 12-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Celniker, S.E., George, R.A., Galle, R.F., Hoskins, R.A.,
Svirskas, R.R., Harris, N.L., Agbayani, A., Arcaina, T.T., Baxter, E.,
Blazej, R.G., Chavez, C., Chew, M., Doyle, C.M., Farfan, D.E.,
Flanagan, J., Houston, K.A., Hummasti, S.R., Karra, K., Kearney, L.,
Kim, S.H., Lee, B., Lomotan, M.A., Mak, J., Mazda, P., Mok, M.S.,
Moshrefi, A.R., Moshrefi, M., Nixon, K., Pacleb, J.M., Park, S.,
Pfeiffer, B., Punch, E., Snir, E., Twomey, B., Wan, K.H., Whitelaw, K.R.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (15-JUL-1998) Berkeley Drosophila Genome Project, 64-121, Lawrence Berkeley National Laboratory, One Cyclotror Berkeley, CA 94720, US Sequence submitted by:
Berkeley Drosophila Genome Project
Lawrence Berkeley National Laboratory, MS 64-121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfeiffer,B., Punch,E., Snir,E., Twomey,B., Wan,K.H., Whitelaw,K.R., Yee,A., Zhang,R., Zieran,L.L. and Kimmel,B.
Sequencing of Drosophila chromosome 2L, region 26C1-26D2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Drosophila melanogaster (Subclones in sac from P1 clones DS00121 (D128), DS05470 (D270), and DS00108 (D120)) DNA.

Drosophila melanogaster
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2 (bases 1 to 209071)
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="DS00121 (d128) extends from bp 1 to bp 84231, DS05470 (d270) extends from bp 64,751 to bp 139,027 an DS00108 (d120) sequenced as a bridge, extends from bp 137,172 to bp 209,071. "
a 45615 c 45383 g 58488 t
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/db_xref="taxon:7227"
/chromosome="2L"
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Pred. No. 1.2e-17;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nagase,T., Ishikawa,K., Nakajima,D., Ohira,M., Seki,N., Miyajima,N., Tanaka,A., Kotani,H., Nomura,N. and Ohara,O. Prediction of the coding sequences of unidentified human genes. VII. The complete sequences of 100 new cDNA clones from brain which can code for large proteins in vitro DNA Res. 4 (2), 141-150 (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nomura, Kazusa DNA Research Institute, Gene Structure 1; 1532-3 Yana, Kisarazu, Chiba 292, Japan (E-mail:cdnainfo@kazusa.or.jp, URL.http://www.kazusa.or.jp, Tel:+81-438-52-3930, Fax:+81-438-52-3931)
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                                                                                                      /translation="MKPLAIPANHGVMGQQEKHSLPADFTKLHLTDSLHPQVTHVSSS HSGCS!TSDSGSSSSLSD1YQATESEAGDMDLSGLPETAVDSEDDDEED1ERASDPLM SRDLTVRDCLEKDF1DATEDD1EGLLEEMHQLBAFANHTMSVYREELCAVWPFAVVERAG TIVLNDGEELDSWSYILNGSVEVTYPDGKAEILCMGNSFGVSPTMDKEYMKGVMRTKV
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63. .4562
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REAPLPFILLGGSEKGFGIFVDSVDSGSKATEAGLKRGDQILEVNGQNFENIQLSKAM
EILRNNTHLSITVKTNLFVFKELLTRLSEEKRNGAPHLPKIGDIKKASRYSIPDLAVD
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/protein_id="BAA20772.1"
/db_xref="GI:2224567"
                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="HG0186"
                                                                                                                                                                                                                                                                                                                                                                       /sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                        LWVNNHFNDFEGDPAMTRFLEEFENNLEREKMGGHLRLLNIACAAKAKRRLMTLTKPS
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                                                                                                                                                                                                                                                                                                                                                                                           /clone_lib="pBluescriptII SK plus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SKOTTAKEVY IQAIREEAVTATPDQYSLCEVSYTPEGYI KQRLIPDQLSKLADRIQLS
GRYYLKNIMETETLCSDEDAQELLRESQISLLQLSTVEVATQRLIBRIFELFRNIEPTE
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     1400 c
1463 g
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Query Match Best Local Match 3.3%; Local Similarity 51.1%; Score 99.2; DB 9; Pred. No. 5.9e-17; Length 6568; BASE CO

COUNT

Matches

289;

Conservative

268;

2

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Search completed: Job time: 32288 se April 22, 2000, 17:50:32

2742

TTTGAGAAGCTAAGGATGATTGCAAA

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Post-processing: Minimum Match 0%
Listing first 45 summaries
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     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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1: /cgn2_6/ptodata/
2: /cgn2_6/ptodata/
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Match
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3013
1 gatccagcgaagatgtggat.....ccacaattttcaaaaatgcc 3013
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    US-08-232-463-14
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1026.159 Million cell updates/sec
 Sequence 6, Appli
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31.8	31.8	31.8	31.8	31.8	31.8	32	32	32	32	32	32	32	32	32	32.2	32.4	32.4
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Sequence 75, Appl	Sequence 222, App	Sequence 2, Appli	Sequence 2, Appli	Sequence 2, Appli	Sequence 11, Appl	•	`	Sequence 90, Appl	`	Sequence 32, Appl	_	Sequence 29, Appl	•	Sequence 32, Appl	•	Sequence 58, Appl	`

ALIGNMENTS

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US-08-232-463-14
                                                                                                                                                               APPLICATION NUMBER: EP 91 114 300.6 FILING DATE: 26-AUG-1991 ATTORNEY/AGENT INFORMATION: NAME: BENT, Stephen A. REGISTRATION NUMBER: 29,768 REFERENCE/DOCKET NUMBER: 30472/114 IMPLECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION: TELEPHONE: (703)836-9300 TELEPHONE: (703)836-9300 TELEPHONE: (703)683-4109 TELEX: 899149 INFORMATION FOR SEQ ID NO: 14:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Patent No. 5670367
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 22313-0299

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Ve

CURRENT APPLICATION DATA:
                             TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
CLONE: pTZgpt-Fls
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road,
                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: UFILING DATE: CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKMER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET:
CITY: A
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               APPLICATION NUMBER: US/08/318,8:
FILING DATE: 19 October 1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: F892/04827
FILING DATE: 21-APR-1992
ATTORNEY/AGENT INFORMATION:
NAME: Smith, Julie K.
REGISTRATION NUMBER: P-38,619
REFERENCE/DOCKET NUMBER: ST9203:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Schweigholter, Eugen APPLICANT: Schweigholter, Eugen APPLICANT: Tocque, Bruno APPLICANT: Tocque, Bruno PEPTIDES HAVING A GDP EXCHANGE FACTOR TITLE OF INVENTION: ACTIVITY, NUCLEIC ACID SEQUENCES CODING TITLE OF INVENTION: PREPARATION AND UTILIZATION

TITLE OF SEQUENCES: 12
                                                                                                                                                                                                                                                                                                                                                           COMPUTER: Macintosh
OPERATING SYSTEM: System 7.1
SOFTWARE: WOID 5.1 (EPO Pater
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Macintosh
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ADDRESSEE: Rhone-Poulenc
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CITY: Collegeville
STATE: PA
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(610)
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3C43
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; LOCATION:
US-08-318-831-1
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Best Local Similarity 42.9
Matches 247; Conservative
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STRANDEDNESS: doub
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TCAACTTCTCCAAGATGAGGATGATATCCCATATTATCCGA
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RESULT 3
US-08-870-518-7
US-08-870-518-7
: Sequence 7, Application US/08870518
; Patent No. 5925566
; GENERAL INFORMATION:
; APPLICANT: Dav1s, Roger J.

2699

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2080

NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:

TITLE OF INVENTION:

PROTEINS AND USES THEREOF

NON-ACTIVATED RECEPTOR COMPLEX

Galcheva-Gargova, Zoya

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US-08-371-377-16
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FILING DATE: 06-JUN-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/019,219
FILING DATE: 06-JUN-1996
ATTORNEY/AGENT INFORMATION:
NAME: Fasse, Peter J.
REGISTRATION NUMBER: 32,983
REFERENCE/DOCKET NUMBER: 04020/1020(
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Fisher,
APPLICANT: Shen, H
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                                                 NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham
STREET: 1185 Avenue of the Americas
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LENGTH: 5183 base pairs
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COMPUTER READABLE FORM:
                                                                                                                      TITLE OF INVENTION: DEVELOPMENT OF DNA PROBES AND
TITLE OF INVENTION: IMMUNOLOGICAL REAGENTS SPECIFIC FOR CELL SURFACE-EXPRESSED
TITLE OF INVENTION: MOLECULES AND TRANSFORMATION-ASSOCIATED GENES
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STRANDEDNESS: single
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 COUNTRY:
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United States of America
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                                                                                                                                                                                           Fisher, Paul B.
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Pred. No. 1
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US-08-371-377-16
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                                                                                                                                                                                                                                                                                                                                                                                          RESULT
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                                                                                                                                                                                                                                                                                                                                       Sequence 1, Patent No.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (212) 391-05
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                      APPLICANT:
APPLICANT:
                                                                                                                NUMBER OF SEQUENCES: 69

CORRESPONDENCE ADDRESS:
ADDRESSEE: Birch, Stewart, Kolasch & Birch
STREET: 301 No. 5728810th Washington Street
CITY: Falls Church
STATE: Virginia
                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                   APPLICANT: Hinman, Michael B.
TITLE OF INVENTION: PROTEIN, A REPLICABLE VECTOR AND A TRANSFORMED CELL
TITLE OF INVENTION: CONTAINING THE ISOLATED DNA, AND PRODUCTS THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                             1693
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELEFAX: (212) 391-0525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1633 TTGATATGGTTCCTGGCAAGCCCATGTGTGTTGAGAGCTTCTCAGACTATCCACCTTTGG 1692
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FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   220 gatgctgtg 228
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM:
COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
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                                                                                                     COUNTRY:
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SYSTEM: PC-DOS/MS-DOS
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Pred. No. 1.1;
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 Version #1.25
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ATTORNEY/AGENT INFORMATION:

FILING DATE: 1: CLASSIFICATION:

19-APR-1995

US/08/425,069

CURRENT APPLICATION DATA:

APPLICATION NUMBER:

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RESULT 6
US-08-317-844B-1
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Best Local Similarity
~~+~hes 85; Conserva
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PAGES: 7120-7124
; DATE: Sept.-1990
; RELEVANT RESIDUES IN SEQ
US-08-425-069-1
                                                                                                                                                                                                                Sequence 1, Application US/08317844B Patent No. 5989894
                                                                                                                                                                                              GENERAL INFORMATION:
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                                                                                     APPLICANT: Lewis, Randolph V.
APPLICANT: Xu, Ming
APPLICANT: Hinman, Michael B.
APPLICANT: Hinman, Michael B.
TITLE OF INVENTION: ISOLATED DNA CODING FOR SPIDER SILK
TITLE OF INVENTION: PROTEIN, A REPLICABLE VECTOR AND A TRANSFORMED CETTITLE OF INVENTION: CONTAINING THE ISOLATED DNA, AND PRODUCTS THEREOF
CORRESPONDENCE ADDRESS:
ADDRESSEE: Birch, Stewart, Kolasch & Birch
STREET: 301 No. 5989894th Washington Street
CITY: Falls Church
                                                                        NUMBER OF SEQUENCES:
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OTHER INFORMATION: dr
PUBLICATION INFORMATION:
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HYPOTHETICAL: NO
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LENGTH: 2338 base pairs
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TELECOMMUNICATION INFORMATION:
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LOCATION: 1...
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AUTHORS: Lewis, Ra
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REGISTRATION NUMBER: 28,977
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Pred. No. 1.2;
0; Mismatches
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                                                       Sequence 17, Application Patent No. 5502166
                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                       Matches
           GENERAL INFORMATION:
APPLICANT: Masayoshi
TITLE OF INVENTION: N
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TELEX: 248345
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 2338 base pairs
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HYPOTHETICAL: N
ORIGINAL SOURCE:
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NAME: Murphy Jr., Gerald
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA: APPLICATION NUMBER: US
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: CDS
LOCATION: 1..2154
OTHER INFORMATION:
OTHER INFORMATION:
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NUMBER OF SEQUENCES:
                                                                                                                                                                                                                  495
                                                                                                                                                                      906 ggatgatccttcgcaaaccacctggccagaggactgtggatgacctaga 954
                                                                                                                                                                                                                                    846 atgaggagctccaggacaccatgctgctgctgtcacagatggccccgacgcccacatga 905
                                                                                                                                                                                                                                                                          435 TGCTGGACAAGGAGGATATGGAGGTCTTGGAAGCCAAGGTGCAGGACGAGGTGGATTAGG 494
                                                                                                                                                                                                                                                                                             786 ttctggatgatgagcacgaggatgcccctttgcctactgaggaggagagaagaaggagtgtg 845
                                                                                                                                                    555 TGGTCTTGGTGGACAAGGTGCCGGACAAGGAGGCTATGGAGGACTTGGA
                                                                                                                                                                                                                                                                                                                                                                                                                             VOLUME: 87
PAGES: 7120-7124
DATE: Sept.-1990
RELEVANT RESIDUES IN SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AUTHORS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (703) 241-2848
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            JOURNAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE: Structure of a protein superfiber: TITLE: drafline silk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 04
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: Virginia COUNTRY: U.S.A.
                                                                                                                                                                                                               TGGACAAGGTGCAGGTGCAGCAGCAGCAGCCGGAGGTGCTGGACAAGGCCGGATACGG 554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        nucleic acid
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Lewis, Randolph V.
                                                                                                                                                                                                                                                                                                                                         Conservative
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50.3%;
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dragline silk protein"
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              PROTEINS
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Pred. No. 1.2;
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              AND GENES
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                                                                                                                                                                                                                                                                                                                                                                    DB 4;
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              CODING
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                                                                                          RESULT 8
US-08-026-138E-6
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                                                           Sequence 6, Application US/08026138E Patent No. 5502166
                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local
         GENERAL INFORMATION:
APPLICANT: MASAYOSHI MISHINA
TITLE OF INVENTION: NOVEL PR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US
FILING DATE: 26 FEB-19
FRIOR APPLICATION DATA:
APPLICATION NUMBER: JF
FILING DATE: 26 FEB-19
APPLICATION NUMBER: JF
FILING DATE: 30-JUN-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (212) 953-7733 INFORMATION FOR SEQ ID NO: 17:
                                                                                                                                                                                                                                                     1132
                                                                                                                                                                                                                      2106
                                                                                                                                                                                                                                                                                     2046
                                                                                                                                                                                                                                                                                                    1072 gtttaaccagggggaagaaggtacctcctggtacattattctaaaaggatcagtgaatgt 1131
                                                                                                                                                                                                                                                                                                                                                                                                                                           PUBLICATION INFORMATION:
AUTHORS: MASSAYOSHI MISHINA
TITLE: NOVEL PROTEINS AND GENES CODING THE
RELEVANT RESIDUES IN SEQ ID NO: 17: FROM 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: JP 215017/1992
FILING DATE: 12-AUG-1992
APPLICATION NUMBER: JP 303878/1992
FILING DATE: 13-NOV-1992
ANTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Word Perfect 5.1 CURRENT APPLICATION DATA:
                                                                                                                                                           2166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 4368 nucleic acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM: MEDIUM TYPE: Diskette,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: mouse
TISSUE TYPE: bra
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                                                                                                                                                                                                                                                                                                                                                               / Match 1.1%;
Local Similarity 54.9%;
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TOPOLOGY: lir
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: nucleic acid
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                                                                                                                                                                                                                                                                                GTTCAACCAAAGGGGTGTAGATGATGCCTTGCTCCCCTGAAAACAGGGAAACTTGATGC 2105
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NOVEL PROTEINS
19
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              AND GENES
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to 43
              CODING
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ORGANISM: MOUSE
TISSUE TYPE: brain
HUBLICATION INFORMATION:
AUTHORS: MASAYOSHI MISHINA
TITLE: NOVEL PROTEINS AND GENES CODING THE SAME
RELEVANT RESIDUES IN SEQ ID NO: 6: FROM 1 to 444
US-08-026-138E-6
                                                                                                                                       US-08-038-682-3
                                                                                                                                                               RESULT
Sequence 3, Application US/08038682
Patent No. 5549897
GENERAL INFORMATION:
APPLICANT: BARENKAMP, STEPHEN J
APPLICANT: ST. GEME III, JOSEPH W
TITLE OF INVENTION: HIGH MOLECULAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
TENGTH: 4446 nucleic acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 26-FEB-1992
APPLICATION NUMBER: JP 173155/1992
FILING DATE: 30-JUN-1992
APPLICATION NUMBER: JP 215017/1992
FILING DATE: 12-AUG-1992
APPLICATION NUMBER: JP 303878/1992
APPLICATION: Hamburg C BRIGG
                                                                                                                                                                                                                               2244
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ORIGINAL SOURCE:
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TELECOMMUNICATION INFORMATION:
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Local Similarity 54.98;
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TOPOLOGY: line
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CITY: Niigata-shi
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Word Perfect 5.1
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212) 953-7733
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Pred. No. 2.
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      WEIGHT SURFACE PROTEINS
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CORRESPONDENCE ADDRESS: NUMBER OF SEQUENCES: TITLE OF INVENTION:

OF NON-TYPEABLE HAEMOPHILUS

2001 Jefferson

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US-08-302-832-3
; Sequence 3, Application US/08302832
; Patent No. 5603938
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TELEPHONE: (703) 415-0813
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 4937 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2239 caaagatttagcataccagatgacaatttatgattgggaactcttcaactgcgtgcatga 2298
                                                                                                                                                                            CORRESPONDENCE ADDRESS
                                                                                                                                                                                                  NUMBER OF SEQUENCES:
                                                                                                                                                                                                                 APPLICANT: Barenkan TITLE OF INVENTION: TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                          2529 GAACATGAACACAAGCAAACCTTTACCAATTCGGTTTTTAGCC 2571
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOTWARE: PATENTIN Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
                                                                                                                             STREET:
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FILING DATE: 16-MAR.
CLASSIFICATION: 424
                                                                      COUNTRY: U.S.A.
                                                                                           CITY: Arlington
STATE: Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: BERKSTRESSER, JERRY W
REGISTRATION NUMBER: 22,651
REFERENCE/DOCKET NUMBER: 10:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 2001
STREET: Bldg.
                                                                                                                                                                ADDRESSEE:
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                                                        22202-0286
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                                                                                                                             Bldg.
                                                                                                                                          E: Shoemaker and Mattare, Ltd.
2001 Jefferson Davis Hwy., 1203 Crystal Plaza
                                                                                                                                                                                                                                                   Barenkamp, Stephen J
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (703) 415-0810
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 Mismatches

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Pred. No. 4.9;
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, 1203 Crystal Plaza
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GENERAL INFORMATION:
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Best Local S
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US pct/us93/02166
FILING DATE: 16-MAR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Berkstresser, Jerry W
REGISTRATION NUMBER: 22,651
REFERENCE/DOCKET NUMBER: 1038-404
TELECOMMUNICATION INFORMATION:
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INFORMATION FOR SEQ ID NO:
                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2469
                                                   CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                        APPLICANT: BARENKAMP, STEPHEN J
APPLICANT: ST. GEME III, JOSEPH W
TITLE OF INVENTION: HIGH MOLECULAR WEIGHT SURFACE PROTEINS
TITLE OF INVENTION: OF NON-TYPEABLE HAEMOPHILUS
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SOFTWARE: PatentIn Rel
CURRENT APPLICATION DATA:
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LENGTH: 4937 base pairs
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APPLICATION NUMBER: GB 9205704.1
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                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                 STREET: 200.
STREET: Bldg. 1
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CITY: Arlington
STATE: Virginia
CLASSIFICATION:
                 APPLICATION NUMBER: FILING DATE: 13-DEC
                                                                                                                                                                                   COUNTRY: U.S.A.
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2001 Jefferson Davis Hwy., 1203 Crystal Plaza
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703) 415-0813
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In Release #1.0, Version #1.30
                                 US/08/530,198
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Pred. No. 4.9;
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SEQUENCE CHARACTERISTICS:
LENGTH: 4937 base pairs
TYPE: nucleic acid
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Best Local Similarity 50.3%;
Matches 82; Conservative
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: PATENTIN Release #1.0.
CURRENT APPLICATION DATA:
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TELECOMMUNICATION INFORMATION:
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NAME: BERKSTRESSER, JERRY W
REGISTRATION NUMBER: 22,651
                                         PILING DATE: 16-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: Berketrocor
                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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APPLICATION NUMBER: (
FILING DATE: 16-MAR-
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PRIOR APPLICATION DATA:
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                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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TELEFAX: (703) 415-0813
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STATE: Virginia
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STREET: Bldg. 1
NAME: Berkstresser, Jerry W
REGISTRATION NUMBER: 22,651
REFERENCE/DOCKET NUMBER: 103
                                                                                                                                APPLICATION NUMBER: FILING DATE: 16-MA
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VENTION: High Molecular Weight Surface Proteins
VENTION: of No. 5876733-Typeable Haemophilus
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06-JUN-1995
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   1038-516 MIS:vg
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Pred. No. 4.9;
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Best Local Similarity 50.38;
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TELECOMMUNICATION INFORMATION: TELEPHONE: (703) 415-0810 TELEFAX: (703) 415-0813
                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9205704.1
FILING DATE: 16-MAR-1992
                                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy
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TELEPHONE: (703) 415-0810
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APPLICATION NUMBER:
FILING DATE: 16-MAR-
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ATTORNEY/AGENT INFORMATION:
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                                                              NAME: Berkstresser, Jerry W
REGISTRATION NUMBER: 22,651
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                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: FILING DATE:
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                                                       REFERENCE/DOCKET NUMBER:
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E: Virginia
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VENTION: High Molecular Weight Surface Proteins
VENTION: of No. 5928651-Typeable Haemophilus
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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101 Jefferson Davis Hwy., 1203 Crystal Plaza
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Pred. No. 4
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US-08-617-697-3
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                  TELEFAX: (703) 415-0813 INFORMATION FOR SEQ ID NO: 3:
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LENGTH: 4937 base pairs
TYPE: nucleic acid
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 08/302,832 FILING DATE: 05-OCT-1994 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/617,697
                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 4937 base pairs
TYPE: nucleic acid
                                                                                                                                TELECOMMUNICATION INFORMATION: TELEPHONE: (703) 415-0810 TELEFAX: (703) 415-0813
                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 01-APR-CLASSIFICATION: 424
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                              FILING DATE: 16-MAR-1993
ATTORNEY/AGENT INFORMATION:
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TOPOLOGY: 11:
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STREET: 2001 Jefferson Davis Hwy., 1203 Crystal Plaza
STREET: Bldg. 1
                                                                                                                                                                                        NAME: Berkstresser, Jerry W
REGISTRATION NUMBER: 22,651
REFERENCE/DOCKET NUMBER: 10
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                      TOPOLOGY:
                                    STRANDEDNESS: single
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16-MAR-1993
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DNA (genomic)
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Best Local
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CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: BERKSTRESSER, JERRY W
REGISTRATION NUMBER: 22,651
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
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TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 415-0810
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                                                 2849 CAAAGGCTTAACAACACAGTATAGAAGCTCTGCAGGGGTGAATTTTAACGGCGTAAATGG 2908
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2299 gctggagctaatctatcacacatittggaaggcataattittaaaaagaccacagcaaacit 2358
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STREET: 2001 Jefferson Davis Hwy., 1203 Crystal Plaza
STREET: Bldg. 1
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                                                                                                                                                                                                                                            STRANDEDNESS:
                                                                                                                                                                                                                                                          LENGTH: 9323 base pairs
TYPE: nucleic acid
                                                                                                                              Local
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                                                                                                                Similarity 50... 82; Conservative
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: Virginia
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ST. GEME III, JOSEPH W
JENTION: HIGH MOLECULAR WEIGHT SURFACE PROTEINS
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Listing first 45 summaries
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Perfect score:
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Copyright (c) 1993 - 2000 Compugen Ltd
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Ehrlichia sp. W20
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Sequence corresp.
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Вb

256 AACCAGAACAGATGTTATATAGATTTCGCTATGATGA 292

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RESULT 3
V21209_12/c
Continuation
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P-PSDB; R91597.
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T13347;
26-JUL-1996 (first entry)
C3G protein gene.
C3G: ras protein guanine nucleotide.
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Sequence 4062 BP; 937 A; 1194 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present sequence encodes C3G protein which is a ras protein nucleotide exchange factor. The gene and protein (see R91597) as
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28-FEB-1995.
13-JUN-1994; 130699.
11-JUN-1993; JP-140806
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Claim 2; Page 6; 9pp; Japanese
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/note= "C3G protein"
of V21209 from base 1200001 (Methanococcus jannaschii circular
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0; Mismatches
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Best Local
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04-JUN-1998;
18-DEC-1997;
06-JUN-1997;
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                                                                                                                                                                                                              Human secreted protein gene 144 clone HGLAM46. Human; secreted protein; fusion protein; gene therapy; protein therapy; diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia; developmental abnormality; foetal deficiency; blood; allergy; renal; ds; immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma; inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS;
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                                                                                                                                                                                cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymu osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion; endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
                                                                                                                                                             Homo sapiens. W09854963-A2.
                                                                                                                                                                                                                                                                                01-MAR-1999 (first entry)
                                                                                                                                                                                                                                                                                                    V84554 standard;
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V21209_01
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             l Similarity
97; Conserv
          US-070923

US-048877.

US-048881.

US-048894.

US-048893.

US-048893.

US-048893.

US-048949.

US-049949.

US-049972.

US-049020.
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PR 05-SEP-1997, US-057638.
PR 05-SEP-1997, US-057647.
PR 05-SEP-1997, US-057647.
PR 05-SEP-1997, US-057661.
PR 05-SEP-1997, US-068878.
PR 06-UNN-1997, US-067662.
PR 06-UNN-1997, US-067663.
PR 06-UNN-1997, US-067663.
PR 06-UNN-1997, US-068878.
PR 06-UNN-1997, US-067663.
PR 06-UNN-1997, US-06
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DR WG 
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Cc geodescriptor line for gene number and clone identification).
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Best Local S
Matches 81
                                                                                          WO9321314-A.
28-OCT-1993.
19-APR-1993; I
21-APR-1992; I
(RHON ) RHONE POULENC RORER Schweighoffer F, Tocque B; WPI; 93-351724/44.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence encoding
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11-MAY-1994 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ttccttttttgccatcgtcatgggactaagtaacattgctgtgagccgcttggcactaac 2562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TCTTTTAAAGGGATAAGGGAATTAGTGGCTTTTAATA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9t999agaaactgccaagcaagttcaagaagttctatgcggagtttgaaagtttaatgga 2622
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      standard;
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                                                                                              F00382.
FR-004827.
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/product= Pe
the p21-GDP
                                                                                                                                                                                                                                                                                                                     /*tag= b
/product= Peptide which
the p21-GDP complex.
976. .2445
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          product= Peptide which modulates GDP exchange
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F; GDP exchange factor; antisense; dia
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Pred. No. 2.
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Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The peptide(s) encoded by the sequence antagonise the interaction of GDP-exchange factor (GRF) with the p21-GDP complex and thereby regulate the activity of ras gene products. They can also be used to identify other compounds which can modulate GDP exchange. The coding sequence can be used to produce antisense products which can inhibit oncogene expression and for use in diagnosis e.g. detecting (over)expression of GRF for typing of cancers.

Sequence 2652 BP; 706 A; 757 C; 629 G; 560 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New peptide(s) modulating GDP exchange in complexes - protein and derived antibodies, nucleic acid etc. esp. diagnosis and treatment of cancer claim 5; Page 16-20, 46pp; French.
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                                                                                                      Sequence corresp. to the g. in clone SIV-1
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                                                                           pSIV-1.1; pSIV-1.2; STLV-III Mac 142-83; Simian immunodeficiency virus.
                                                                                                                                                       N80860;
15-NOV-1990 (first
                                                                                                                                                                                              N80860
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                                                                                                                                                                                                                                                                                                                                                                           ACCTCACCGACCTGGCCTTCATCGAGGAGGGGACGCCCAATTACACGGAAGACGGCCTGG
                                                                                                                                                                                              standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
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                                    Location/Qualifiers 551. .2068
                                                                                                                                                                                                cDNA;
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                                                                                                                                      genome
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Pred. No. 2
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P-PSDB; P80802, p81783, p81784, p81785, p81691, p81756, p81757, p81758, p8 p81759, p81760, p81761, p81762.

PR p81759, p81760, p81761, p81762.

PR New peptide(s) with immunological properties of HIV-2 envelope protein protein the structure of similar immune deficiency virus proteins, protein in diagnosis and of vaccine components

Pr Laim 23; Fig 1B; 86pp; French.

Pr Claim 24; Fig 1B; 86pp; French.

Pr Claim 24; Fig 1B; 86pp; French.

Pr Claim 25; Fig 1B; 8
                         Query Match
Best Local
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Alizon M, Montagnier L, Gue
Tiollais P, Chakrabarti L,
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28-JUL-1988.
15-JAN-1988; F00025.
15-APR-1987; FR-005398,
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                                                                                                                                  treatment of AIDS. Sequence 9601 BP;
                                                                                                                                                                                     vaccines against HIV. Antibodies raised
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Similarity
60; Conser
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/gene="Q"
5298. .5633
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5637. .5939
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/gene="art1"
6090. .8297
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/*tag= b
/gene="pol"
4826. .5467
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8294. .8548
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6014. .6130
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                            1.2%;
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- f
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Score 35.4; D
Pred. No. 6.3;
0; Mismatches
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                            35.4;
No. 6
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                                                     BB
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                                                                                                                                       G;
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gttcttttgcaacagttcaatacgggcgatgagagagccca

TTGGAGGCAAATATAACGGCCCTCCTAGAAGAGGCACAAATTCAACAAGAAGAACATG

Conservative

0;

41;

0

Gaps

0

8094

밁

metastasis;

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RESULT
T37405
                                                                                                                                                                                                                                                                                                                                                                                                                                                           C belongs to a novel class of signalling molecules (see also

W M8454-57) that bind to non-activated receptors (e.g. EGF and pDGR

C receptors) and specifically bind small nucleolar RNAs (e.g. U3).

C Saccharomyces cerevisiae, S. pombe and human EPRI clones (see

V 04062-64) were identified using a mouse ZRP1 clones (see

V 04062-64) were identified using a mouse ZRP1 clone (see

V 04062-64) were identified using a mouse ZRP1 clone (see

V 04062-64) were identified using a mouse ZRP1 clone (see

V 04061) as

C cells. ZPR1 is expressed at an elevated level in tumour derived

C cells, and is a marker for growth and differentiation processes,

C including malignant transformation of cells. ZPR1, optionally

C expressed by gene therapy methods, can be used to inhibit the

C proliferation of ZPR1 associated malignant cells, or for the

C expression. Suppressors and modulators of ZPR1 gene

expression. Suppressors and modulators of ZPR1 gene

c angiogenesis, e.g. to treat tumours, diabetic retinopathy,

rheumatoid arthritis, psoriasis and coronary atheroma, and/or

increase tubular reageneration of the following active
                                                                                                                                                                                                                                                                                                                               Query Match
Best Local S
Matches 70
       T37405 standard; cDNA; 2128 T37405;
                                                                                                                                                                                                                        2638
                                                                                                                                                                                                                                                           1970
                                                                                                                                              2698 gctcatta 2705
                                                                                                                                                                                                                                                                        2578 aagcaagttcaagaagttctatgcggagtttgaaagtttaatggacccttcaaggaacca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nucleic acid sequence encoding RNA-binding polypeptide ZRP1 - useful to reduce anglogenesis, increase cell proliferation or kidney cell regeneration or inhibit tumour growth Claim 9; Fig 6; 88pp; English.

This nucleotide sequence comprises a cDNA clone coding for Schizosaccharomyces pombe ZRP1 (see W38456), a novel protein that
                                                                                                              2090 GGACTTGA 2097
                                                                                                                                                                                                                                                                                                                                                                                                                  increase tubular regeneration of kidney cells, e.g. following renal failure.
Sequence 5183 BP; 1629 A; 906 C; 993 G; 1655 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZPR1; RNA-binding protein; non-activated receptor complex; signal transduction; epidermal growth factor receptor; platelet derived growth factor receptor; receptor; angiogenesis; diahetic retinocath.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (UYMA-) UNIV MASSACHUSETTS
Davis RJ, Galcheva-Gargova
WPI; 98-042192/04.
P-PSDB; W38456.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     angiogenesis; diabetic retinopathy; rheumatoid arthritis; psoriasis; coronary atheroma; renal failure; gene therapy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               08-JUN-1998 (first entry)
Schizosaccharomyces pombe RNA-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8095 TATGAATTACAAAAGTTGAATAGCTGGGATGTGTTTGGCAA 8135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                06-JUN-1997; U09911
06-JUN-1996; US-019
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                                                                                                                                                                                                 cagggcctacaggctgacagtagctaagctggaacctcctctcatccccttcatgccttt
                                                                                                                                                                              GAGGACTTATCCCGTGATATTCTCAAATCTGAAACCGCATCTCTTAAAATTCCTGAACTT
                                                                                                                                                                                                                                                    AAGACTGGTGGTGAAATTCCACCCAAAGGTCGAAAAATTACTTTAAAGGTCATGGATGCC
                                                                                                                                                                                                                                                                                                                               l Similarity
70; Conserv
                                                                                                                                                                                                                                                                                                                               Conservative
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Pred. No. 4.9;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                           Length 5183;
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Q14183
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Best Local S
Matches 70
                                                      15-JAN-1992 (first entry)
N.clavipes dragline silk protein coding sequence protein superfibre; major ampullate silk; orb wel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             human prostatic carcinoma LNCaP cell DNA-transfected tumour-derived murine CREF-Trans 6 cells using an RNA differential display method, and full-length cDNA can be directly cloned from an LNCaP cDNA library. The PTI-1 gene comprises a unique 5 630 bp region and a 3 truncated and mutated elongation factor-1 alpha gene. It codes for a 46 kDa protein (W03518). PTI-2 (T37412), PTI-3 (T37413) and a prostate carcinoma tumour antigen gene (T37414) were also identified. The PTI-1 gene can be used to design probes useful e-9. for detection of metastatic cancer, or to produce recombinant proteins. Antisense sequences can be used in cancer therapy. Sequence 2128 BP; 608 A; 434 C; 536 G; 550 T;
                                              Nephilia clavipes.
                                                                                                   Q14183;
15-JAN-1992
                                                                                                                                     Q14183 standard; cDNA; 2338
                                                                                                                                                                                                                               1693
                                                                                                                                                                                                                                                                                             1633 TTGATATGGTTCCTGGCAAGCCCATGTGTGTTGAGAGCTTCTCAGACTATCCACCTTTGG
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11-JAN-1996; U00307.
11-JAN-1995; US-371377.
(UYCO) UNIV COLUMBIA NEW YORK.
Fisher PB, Shen R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Prostate tumour inducing gene-1 (PTI-1) (T37405) is a novel putative oncogene that may contribute to carcinoma development in human prostate and other tissues. PTI-1 was initially identified in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA encoding prostate carcinoma tumour antigen and prostate tumour inducing genes - and related proteins, vectors, antibodies, etc., for diagnosis and treatment of metastatic cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26-NOV-1996 (1115- ......)

Prostate tumour inducing gene-1; PTI-1; oncogen

Prostate tumour inducing gene-1; PTI-1; oncogen

elongation factor-1 alpha; diagnosis; therapy;

elongation factor-1 alpha; diagnosis; ss.
                                                                                                                                                                                                                                                                   220
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                                                                                                                                                                                                                               GCTGCTTTG 1701
                                                                                                                                                                                                                                                      gatgctgtg
                                                                                                                                                                                                                                                                                                                      ctggtatgctgcctggcagggtctttggatgttaaagtatctgagaccagcagcagtcaccag 219
                                                                                                                                                                                                                                                                                                                                                                   GTTCTGGTAAAAAGCTGGAAGATGGCCCTAAATTCTTGAAGTCTGGTGATGCTGCCATTG 1632
                                                                                                                                                                                                                                                                                                                                                                                         gttattatgagaatctggaaaagggaataacattatttcgccagggtgatatggaacaaa 159
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             Location/Qualifiers
1. .2157
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/note= "A p
621. .1817
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/note= "L
567. .586
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/note= "ACC encodes Thr"
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Pred. No. 4.
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DB

Length 2128; Indels

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Gaps

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orb web spider;

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RESULT
V23249
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Spider; Nephila clavipes; silk v
cocoon; tensile strength; elasti
Nephila clavipes.
Key Location/On-214-64
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Best Local
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23-CCT-1991; 106217.
18-APR-1990; US-511792.
20-APR-1990; US-511792.
(UYWY-) UNIV OF WYOMING.
Lewis RV, Xu M, Hinman M;
WPI; 91-312199/43.
P-PSDB; R14308.
                                                                                                                                                                                        US5728810-A.
17-MAR-1998.
19-APR-1995; 425069.
15-APR-1991; US-684819.
20-APR-1999; US-511792.
04-OCT-1994; US-317844.
19-APR-1995; US-425069.
(UYWY-) UNIV WYOMING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA encoding spider silk protein-1 and 2 and variants - isolated from Nephila clavipes, for prodn. of spider silk protein and fibres having desired characteristics Claim 4; Page 23; 48pp; English.

A N.clavipes major ampullate gland cDNA library was screened with probes based on peptide fragments of the purified spider silk protein (see Q14185). Positive plaques were identified and the spider silk protein 1 coding sequence was determined. See also Q14184.
          Recombinant spider silk proteins - useful for making fibres Example 3; Column 25-30; 68pp; English.

The present sequence encodes a spider silk protein from the present invention. Spider silk proteins, and peptide fragments within the proteins, can be produced and purified independently and can then be mixed and made into fibres that have higher tensile strengths and elasticity than naturally occurring fibres. The fibres can be used in mixed composites. The invention allows the two naturally occurring weightla clavipes silk proteins to be produced independently so that they can later be combined to form silk fibres of high tensile strengths.
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98-270437/24.
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                                                                                                                                                                                                                                                                                                                                                                       clavipes spider silk protein enc
Nephila clavipes; silk protein;
tensile strength; elasticity; ss
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                                                                                                                                                                           This sequence encodes two proteins which are associated with granulocytic ehrlichia (GE), W20.1 and W20.2 which have been isolated from HL60 cells infected with Ehrlichia sp. GE is an acute potentially fatal tick borne infection and the proteins described in this invention can be used in vaccines to elicit a beneficial immune response in an animal to GE. They can be used for inhibiting Ehrlichoisis in an animal The products can also be used for detection and diagnosis. Sequence 4833 BP; 1484 A; 797 C; 1114 G; 1438 T;
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New isolated granulcytic erhlichia nucleic acids - used to products for use in vaccines for inhibiting Ehrlichiosis an in detection and diagnosis

Claim 2; Fig 1; 184pp; English.
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05-NOV-1998.
24-APR-1998; U08264.
25-APR-1997; US-044869.
(AQUI-) AQUILA BIOPHARMACEUTICALS BELTZ G, COUGHAIN RT, MURPHY C, St
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Ehrlichia sp. W20 genomic D
Granulocytic ehrlichia; GE;
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Staphylococcus aureus contig SEQ ID #164.

Computer readable medium; vaccine; S.aureus infection; immunodetection; ceilulitis; eyelid infection; food poisoning; osteomyelitis; therapy; skin infection; surgical wound infection; scalded skin syndrome;
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that protein encoding or regulatory regions of commercial, therapeutic or industrial importance can be obtained. Specifically, sequences which are likely to encode antigens have been identified and these polypeptides can be used in a vaccine composition against S aureus infection. The polypeptides can also be used in a kit for the immunodetection of S aureus in a sample. Saureus is implicated in numerous human diseases, including cellulitis, eyelid infections, food poisoning, osteomyelitis, skin and surgical wound infections, scalded skin syndrome, toxic shock syndrome, etc. Organisms transformed with the DNA sequences can be used for recombinant production of the polypeptides. The new DNA sequences (and their fragments) are useful as primers or probes for isolating homologues of any of the S.aureus DNA sequences contained on the computer readable medium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            of the invention. The DNA sequences are recorded on a computer reada medium, preferably selected from a floppy or hard disk, random access memory (RAM), read-only memory (ROM) or CD-ROM. Homology searches us the S.aureus DNA sequences allows putative functions to be assigned
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 anti-S.aureus vaccines
Claim 1; Page 800-813; 3271pp; English.
This sequence represents one of 5191 Staphylococcus
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07-JAN-1997; 100117.
05-JAN-1996; US-009861.
(HUMA-) HUMAN GENOME SC
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04-SEP-1997:
04-SEP-1997:
08-FEB-1997:
003156.
20-MAY-1996: US-650766.
01-MAY-1996: US-012600.
(UMIS ) UNIV MISSISSIPPI M
IVANOV TR, PILETZ JE;
WPJ: 97-448631/41.
                                                                                                                                                              11-MAR-1999.
03-SEP-1997;
03-SEP-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This sequence represents cDNA encoding a human imidazoline type 1 receptor (IR1), which has 559 (full length) or 298 (breakdown product) amino acid residues. The protein is highly unique in its sequence and may represent the first in a novel family of receptor proteins. The cDC can be used to produce recombinant IR1, to screen for ligands binding IR1, to raise antibodies against IR1 or to probe for other genes encoded beginning to the contraction.
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Nucleic acid encoding imidazoline receptor subtype 1 -
screening for (ant)agonist, homologous receptors, etc.
Claim 10; Pages 49-50; 72pp; English.
                                                                                           03-SEP-1997; U15695.
03-SEP-1997; WO-U15695.
(UMIS ) UNIV MISSISSIPPI
IVANOV TR, Piletz JE;
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Pred. No. 4.3;
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:: 594. .596, aa:Trp)
:: 610. .612, aa:Trp)
:: 646. .648, aa:Trp)
:: 1003. .1005, aa:Trp)
:: 1199. .1092, aa:Trp)
:: 1147. .1119, aa:Trp)
:: 1177. .1179, aa:Trp)
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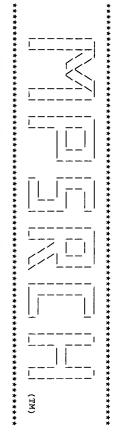
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA material encoding polypeptides that are receptive to imidazoline compounds. The isolation of polynucleotides encoding the imidazoline receptive polypeptides have immunological and ligand binding properties, which enable identification of agents having greater potency and/or more selectivity for these receptors.

Sequence 1954 BP; 367 A; 645 C; 591 G; 351 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  receptive polypeptides (Claim 2; Page 59-60; 102pp; English. This sequence encodes an imidazoline receptor of the invention. Host cells expressing the polypeptides are useful for screening for ligands of an imidazoline receptor. Restriction fragments of the polynucleotide are useful as labeled probes for isolating and identifying
screening for (ant)agonist, homologous receptor Claim II; pages 50-52; 72pp; English.
This sequence represents cDNA encoding a human receptor (IR1), which has 559 (full length) or
                                                                                                               Ivanov TR, Piletz JE;
WPI; 97-448631/41.
P-PSDB; W43396.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human imidazoline receptor subtype 1 Imidazoline receptor subtype 1; IR1; antibody; C-terminal fragment; ds.
                                                                                          Nucleic acid encoding
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                                                                                           2211
                                                                                                                                                                 2151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            amino acid residues. The protein is highly unique in its sequence and may represent the first in a novel family of receptor proteins. The cDNA can be used to produce recombinant IRL, to screen for ligands binding IRL, to raise antibodies against IRI or to probe for other genes encoding homologous IRI proteins.

Sequence 3317 BP; 721 A; 961 C; 948 G; 687 T;
                                                                                                                                                                                                                                         2091
                                                                                                                                                                                                                                                                                                         2031 CAGGGCGAGGAGGATGAGGAGGAGGAGGAGGAGGACGTGGCTGAGAACCGCTAC 2090
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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Sat Apr 22 13:20:48 2000; MasPar time 123.15 Seconds 477.985 Million cell updates/sec

Tabular output not generated.

Title: >US-09-422-999-18 (1-849) from US09422999.pep 6222

Description: Perfect Score: Sequence: 1 MVLWKRALTMTGFLTRRTHL.....VIDNQRTLSQMSHRLEPRRP 849

Scoring table: PAM 150 Gap 11

Post-processing: Minimum Match 0% Listing first 45 summaries Searched: 225878 seqs, 69334122 residues

Database:

sptremb112
1:sp_archea 2:sp_bacteria 3:sp_fungi 4:sp_human
1:sp_archea 2:sp_bacteria 7:sp_mhc 8:sp_organelle
5:sp_inage 10:sp_plant 11:sp_rodent 12:sp_unclassified
13:sp_vertebrate 14:sp_virus

Statistics: Mean 53.509; Variance 96.380; scale 0.555

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

1 3 3 4 4 3 3 5 5 6 6 7 7 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	Result
6038 5835 3052 2942 2946 2820 1177 595 595 3870 370 370 370 370 370 370 370 370 370 3	Score
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NEUROPATHY TARGET ESTE	ZK742.1 PROTEIN.	HYPOTHETICAL 71.2 KD P	SIMILARITY TO REGIONS	HYPOTHETICAL 110.2 KD	PUTATIVE VOLTAGE-AND C	CYCLIC NUCLEOTIDE AND	CATABOLITE GENE ACTIVA	HRSH2.	44 KDA REGULATORY SUBU	CALCIUM AND DAG-REGULA	RAS GUANYL RELEASING P	RAS ACTIVATOR RASGRP.	F25B3.3 PROTEIN.	CAMP PROTEIN KINASE RE	REGULATORY SUBUNIT OF	CAMP-DEPENDENT PROTEIN	F25B3.3 KINASE LIKE PR	RET TYROSINE KINASE/CA	SIMILAR TO CAMP-DEPEND	FYVE FINGER-CONTAINING	MAT LOCUS GENES BUD5,	CYCLIC NUCLEOTIDE BIND	CAMP-DEPENDENT PROTEIN	KIAA0846 PROTEIN.	
5.93e-06	8.50e-06	1.22e-05	4.13e-06	2.87e-06	1.04e-07	2.19e-07	1.08e-08	3.43e-09	1.59e-09	4.74e-11	4.74e-11	4.74e-11	3.19e-11	7.02e-11	7.02e-11	2.28e-10	9.71e-12	1.31e-12	1.96e-12	3.42e-14	7.73e-14	7.73e-14	ā	5.52e-16	

ALIGNMENTS

DЬ	Оу	DЬ	рь Оу	рь Оу	Query Best Match		ID O
420 DFGKLALVNDAPRAASIVLREDNCHFLRVDKEDFNRILRDVEANTVRLKEHDQDVLVLEK 479	360 LSTTVKRELAGVLIFESHAKGGTVLFNQGEEGTSWYIILKGSVNVVIYGKGVVCTLHEGD 419 	300 PTEEEKKECDEELQDTMLLLSQMGPDAHMRMILRKPPGQRTVDDLEIIYEELLHIKALSH 359 	240 ELVDWMMQQTPCVHSRTQAVGMWQVLLEDGVLNHVDQEHHFQDKYLFYRFLDDEHEDAPL 299 :::	180 TPLIEDHVPLRPANTITKVPSEKILRAGKILRNAILSRAPHMIRDRKYHLKTYRQCCVGT 239 	Query Match 97.0%; Score 6038; DB 4; Length 1011; Best Local Similarity 99.4%; Fred. No. 0.00e+00; Matches 827; Conservative 3; Mismatches 2; Indels 0; Gaps 0;	; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ;	O95636 PRELIMINARY: PRT: 1011 AA.

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PRELIMINARY; PRT; 993 AA.

09Z1P0;
01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
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musculus (Mouse).
Chordata;
                                                                                                                                      KVVLKPNDVSVFTTLTINGRLFACPREQFDSLTPLPEQEGPTVGTVGTVFELMSSKDLAYQ
DKYLFYRFLDDEREDAPLPTEEEKKECDEELQDTMLLLKSQMGFDAHMRMILRKPPGQRTV
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                                                                    IRDRKYHLKTYRQCCVGTELVDWMIQQTSCVHSRTQAVGMWQVLLEDGVLNHVDQERHFQ
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795; Conser
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93.5%;
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Pred.
28; M
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0921C7;
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01-MAY-1999 (TIEMBLIEL 1
01-MAY-1999 (TIEMBLIEL NU
            EMBL; U7
                   KAWASAKI H., SPRINGETT G.M., MATSUDA M., HOUSMAN D.E., GRR.
"A family of cAMP-binding proscience 282:2275-2279(1998).
EMBL; U78517; AAD03423.1; "NOW TEN
                                                                          SEQUENCE FROM N.A.
STRAIN-SPRAGUE-DAWLEY;
MEDLINE; 99074384.
                                                                                                                   Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chor
Eutheria; Rodentia; Sciu
                                                                                                                                                        CAMP-GEFII.
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Sciurognathi; Muridae;
 50117 MW;
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. NUCLEOTIDE EXCHANGE FACTOR II
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095398;
01-MAY-1999
01-MAY-1999
01-NOV-1999
                                                                                                                                                                                                                                                               MEDLINE; 99068645.

DE ROOLJ J., ZWARTKRUIS F.J.T., VERHEIJEN M.

NIJMAN S.M. B., WITTINGHOFER A., BOS J.L.;

"Epac is a Rapl guanine-nucleotide-exchange by cyclic AMP.";

Nature 396:474-477(1998).

EMBL; AF103905; AAC83381.1; -.

HSSP; P00515; 2BPK.
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01-MAY-1999 (TrEMBLrel. 10, Last sequence up
01-NOY-1999 (TrEMBLrel. 12, Last annotation
RAP1 GUANINE-NUCLEOTIDE EXCHANGE FACTOR.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vert
                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=MUSCLE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eutheria; Primates;
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Local :
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                                                                             QRTLSQMSHRLEPRRP 436
                           GRELVDGILALGLGVHSRSQVVGICQVLLDEGALCHVKHDWAFQDRDAQFYRFPGPEPE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EGNKTFIDNLVNFEKMRMIANTARTVRYYRSQPFNPDAAQANKNHQDVRSYVRQLNVIDN
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larity 51.1%;
Conservative
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larity 95.6%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chordata; Craniata; Vertebrata;
                                                                                                                                                                                                                                                MW;
                                                                                                                                                            Score 2942; DB 4;
Pred. No. 0.00e+00;
189; Mismatches 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 3052; DB 11;
Pred. No. 0.00e+00;
10; Mismatches 9;
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BOS J.L.;
                                                                                                                                                              Mismatches 188;
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Query Match
Best Local Similarity
                                                          SEQUENCE FROM N.A.

MEDLINE; 99074384.

KAWASAKI H., SPRINGETT G.M., MATSUDA M., HOUSMAN D.E., GRAY

"A family of cAMP-binding prot
"Campene 282:2275-2279(1998).

EMBL; U78168; AAD12740.1; -.

HSSP; P00515; 2BPK.

SEQUENCE 881 AA; 99376 MW;
                                                                                                                                                                                                                                                                                                O95634;
O95634;
O1-MAY-1999 (TIEMBLIEL. 10, Created)
O1-MAY-1999 (TIEMBLIEL. 10, Last sequence update)
O1-NOV-1999 (TIEMBLIEL. 12, Last annotation update)
O1-NOV-1999 (TIEMBLIEL. 12, Last annotation update)
                                                                                                                                                                                                                                                                               Homo sapiens (Human) Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                 Eutheria;
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2 IANTARTVRYYRSQ
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Catarrhini;
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  Score
Pred.
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2936; DB 4;
No. 0.00e+00;
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0721C8 PRELIMINARY; PRT; 884 AA.
0721C8;
01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
CAMP-REGULATED GUANINE NUCLECTIDE EXCHANGE FACTOR I
                         CAMP-GEFI.
Rattus norvegicus (Rat).
               Eukaryota;
Eutheria; F
     SEQUENCE
 MEDLINE;
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2 IANTARTVRYYRSQ
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                                                                                                                                                                                                                                                                                                       -PVGTHE--ME--EELAEAVALLSQRGPDALLTVALRKPPGQRTDEELDLIFEELLHIKA
                                                                                                                                                                                                                                                                                                                           EGDDFGKLALVNDAPRAASIVLREDNCHFLRVDKEDFNRILRDVEANTVRLKEHDQDVLV
                                                                                                                                                                                                                                                                                                                                                                   404;
 99074384
                Rodentia;
                    Metazoa;
                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                         816
               Chordata; Craniata; Ve
Sciurognathi; Muridae;
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                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                    Vertebrata;
                Murinae;
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               Mammalia;
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PRELIMINARY;

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KAWASAKI H., SPRINGETT G.M., MOCHIZUKI N., TOKI S MATSUDA M., HOUSMAN D.E., GRAYBIEL A.M.;
"A family of camp-binding proteins that directly Science 28:2275-2279(1998).
Science 28:2275-2279(1998).
EMBL; U78167; AAD12739.1; -.
HSSP; P00515; ZBPK.
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                          MRMMARAVRMLHHCRSHSTAP
                                                                                                        GRELVDGILALGLGVHSRSQAVGICQVLLDEGALCHVKHDWTFQDRDAQFYRF-PG-PE-
                                                                    KLYSALERLLDPSWNHRVYRLALTKLSPPVIPFMPLLLKDMTFIHEGNHTLVENLINFEK
                                                                                                                                                                                                            VKMSSGGEKVVLKPNDVSVFTTLTINGRLFACPREQFDSLTPLPEQEGPTVGTVGTFELM
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MRMIANTARTVRYYRSQPFNP
                                                      KFYAEFESLMDPSRNHRAYRLTVAKLEPPLIPFMPLLIKDMTFTHEGNKTFIDNLVNFEK
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ilarity 50.1%;
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Pred. No. 0.00e+00;
186; Mismatches 200;
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O9Y4GB;
O1-NOV-1999 (TIEMBLIEL 1
O1-NOV-1999 (TIEMBLIEL 1
O1-NOV-1999 (TIEMBLIEL 1
KIAAO313 PROTEIN.
KIAAO313;
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Eukaryota; Metazoa;
Eutheria; Primates;
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01-NOV-1998 (TrEMBLrel.
MYELOBLAST KIAA0277.
KIAA0277.
Homo sapiens (Human)
Eukaryota; Metazoa;
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PF00617; RASGEF; 1.
PF00618; RASGEFN; 1.
NCE 580 AA; 67733 MW;
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Similarity 47.3%; Pred. No. 0.00e+00;
245; Conservative 125; Mismatches 138;
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imates; Catarrhini; Hominidae; Homo.
  Chordata;
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Q21218; Q22503;
Q21218; Q22503;
Q1.NOV-1996 (TrEMBLrel. 0:
Q1-MAY-1999 (TrEMBLrel. 1:
Q1-MAY-1999 (TREMBLrel. 1:
T14G10.2 PROTEIN.
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NAGASE T., ISHIKAWA K., NAKAJIMA D., OHIRA M., SEKI N., MIYAJIM TANAKA A., KOTANI H., NOMURA N., OHARA O.;

"Prediction of the coding sequences of unidentified human genes The complete sequences of 100 new cDNA clones from brain which code for large proteins in vitro.";

DNA Res. 4:141-150(1997).

EMBL; AB002311; BAA20772.1; -.

SEQUENCE 1499 AA; 167416 MW; D7CB0593 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eutheria; Primates; Catarrhini;
[1]
                                                                                                                                                                                                                           EMBL;
EMBL;
EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                         Caenorhabditis elegans.
Eukaryota; Metazoa; Nemato
Rhabditina; Rhabditoidea;
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PL-PEQEGPTVGTVGTVGTELMS-SKDL-AYQMTIYDWELFNCVHELELIYHTFGRHNFKKT 647
                           PLVPDELAPELLKEAQTQLLSLNAQVVAAQLTLQDFSVFSAIEPTEFLDNLF-KLDSKYG
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                                                                                                                                                                                                                        Z69664; CAA93519.1; JOINED. Z68880; CAA93519.1; JOINED. Z68880; CAA93100.1; JOINED. Z69664; CAA93100.1; JOINED.
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llarity 36.6%;
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larity 36.3%;
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                                                                                                                                                                                             00.1; JOINED.
144639 MW;
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Pred. No. 5.32e-97;
78; Mismatches 101;
                                                                                                 Pred. 71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Created)
Last sequence update)
Last annotation updat
                                                                                                                            Score 555; DB 5;
Pred. No. 3.20e-88;
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C Olganis (Human)
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023867;
023867;
01-NOV-1996
01-NOV-1998
                             TANAKA S.
      Submitted
                                                                                          TISSUE-SPLEEN, A
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larity 27.5%;
Conservative
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; Dictyostelium.
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Last sequence update)
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Pred. No. 2.36e-51;
67; Mismatches 73;
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KNUDSEN B., FELLER S., HANAFUSA H.;
"Four proline-rich sequences of the C3G bind with unique specificity to CTK.";
                                                                                                                                                                                          CONNOLLY K.S., GUNNING K.M., DAVIS C.A., KADNER K., SUBRAMANIAN S., MIGUEL T., LEWIS K.D., FRIDLYAND J., ALCIVARE D., BENKE J.A., BONDEC M., BOWED E., CHIANG A., CRITZ P., JAKLEVIC M.A., LINDO K., LINDQUIST K., MILLER C., PATEL S., PISCIA C., RILEY B.E., ROJESKI H., SARMIENTO R., YU C., MONTENEGRO M., AERTS A., CHUNG A., ABRAJANO A., BAKER M., GAU C., JETT J., KO C., BEALL K., MOOLLEY J.P., STULTZ J.L., KIMMERLY W., MARTIN C.H.,
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SEQUENCE FROM N.A.
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SEQUENCE FROM N.A.
TISSUE=SPLEEN, AND
                       SEQUENCE FROM N.A. RICKE D.O., WAGNER R.P.; RICKE D.O., WAGNER R.P.; Submitted (FEB-1998) to the EMBL; AC004227; AAC04379.1; HSSP; P31016; 1BFE.
                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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01-JUN-1998 (TrEMBLrel.
01-NOV-1999 (TrEMBLrel.
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     PF00027;
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                                                                                                                                                                     W., MARTIN C.H.
(FEB-1998) to
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cNMP_binding;
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Pred. No. 1.20e-48;
52; Mismatches 77;
                                                                           EMBL/GenBank/DDBJ
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Best Local Similarity 26.9%;
Matches 66; Conservative
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Best Local Similarity 32.8%;
Matches 60; Conservative
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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TER 1237 1237
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FMGNSFGITPTLDKQYMHGIVRTKVDDCQFVCIAQQDYWRILNHVEKNTHKVEEBGGIVM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ALSHLSTTVKRELAGVLIFESHAKGGTVLFNQGEBGTSWYIILKGSVNVVIYGKGVCTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DAPLPTEEEKKECDEELQDTMLLLSQMGPDAHMRMILRKPPGQRTVDDLEIIYEELLHIK 193
     EPRRP
                                                  EPRLP 1236
                                                                                                  NFEKMRMIANTARTVRYYRSQPFNPDAAQANKNHQDVRSYVRQLNVIDNQRTLSQMSHRL
                                                                                                                               NFSKMRMISHIIREIRQFQQTSYRIDH-QP-KVAQYLLD--KDL-IIDED-TLYELSLKI 1231
                                                                                                                                                                                                 KFKKFYAEFESLMDPSRNHRAYRLTVAKLEPPLIPFMPLLIKDMTFTHEGNKTFIDN-LV
                                                                                                                                                                                                                                              QTKALMDKLQKTVSSEGRFKNLRETLKNCNPPAVPYLGMYLTDLAFIEEGTPNFTEEGLV
                                                                                                                                                                                                                                                                                                                                                                                              FELMSSKDLAYQMTIYDWELFNCVHELELIYHTFGRHNFKKTTANLDLFLRRFNEIQFWV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AF023130; AAB80953.1;
PF00612; IQ; 1.
PF00169; PH; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PF00595; PDZ; 1.
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579
579 AA;
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65197 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 326; DB 4; Length 123
Pred. No. 1.32e-39;
72; Mismatches 100; Indels
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Last sequence update)
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Pred. No. 1.02e-44;
56; Mismatches 61;
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RESULT 14

RESULT 14

RESULT 17

RAC 970392;

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DT 01-FEB-1997 (
DT 01-NOV-1999 (
DT 01-NOV-1997 (
DT 01-NOV-1997 (
DT 01-NOV-1997 (
DE RAS PROTEIN-S

CR RAS PROTEIN-S

CR LAS-GRE2).

GN RASGRE2.

OS MAS MUSCULUS

CR LUKARYOCA; ME

COC EUKARYOCA; ME

COC EUKARYOCA; ME

CHEN L., ZHAN

RT NA MEDLINE; 9412

RA CHEN L., ZHAN

RT PAM LEPOLINE; 9711

RN (2)

RP SEQUENCE FRON

RC TISSUE-BRAIN,

RY MEDLINE; 9711

RN SECUENCE; PAM N.P., FAM

RT "Cloning and

RT AM N.P., FAM

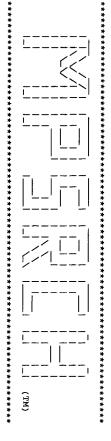
RT MOD. Cell. B.

DR EMBL; U67336

DR PAM; PF0061

DR PFAM; PF0061
RESULT
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Best Local 9
                             015059
015059;
01-JAN-1998
01-JAN-1998
01-NOV-1998
KIAA0351.
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PFAM; PF00169; E
PFAM; PF00617; F
PFAM; PF00618; F
PFAM; PF00621; F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Cloning and characterization of Ras exchange factor for Ras."
MO1. Cell. Blol. 17:1396-1406(1997).
EMBL: 067326; AAC53058.1; --
MGD; MG1:109137; Rasgrf2.
PFAM; PF00612: TO: 1
KIAA0351.
Homo sapi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE; 94123458.
CHEN L., ZHANG L.J., GREER P., TUNG P.S., MORAN M.F. A murine CDC25/ras-GRF-related protein implicated
                                                                                                                                                                                                                                                                                                                                             1070
                                                                                                                                                                                                                                                                                                                                                                                                 1010 ASQIMNYADISSRPNAIEKWYAVADICRCLHNYNGVLEITSALNRSPIYRLKKTWAKVSK 1069
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                              1130
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Dev. Genet. 14:339-346(1993).
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                                                                                                                                                                              845
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FEB-1997 (TrEMBLrel. 02, Last sequence update)
NOV-1999 (TrEMBLREL. 12, Last annotation update)
PROTEIN-SPECIFIC GUANINE NUCLEOTIDE-RELEASING F
                                                                                                                                                                                                                                           NFSKMRMISHIIREIRQFQQTAYRIDQ-QP-KVIQYLLD--KAL-VIDED-SLYELSLKI 1183
                                                                                                                                                                                                                                                                                                                                  QTKALMDKLQKTVSSEGRFKNLRETLKNCNPPAVPYLGMYLTDLAFIEEGTPNFTEEGLV
sapiens
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Similarity 26.9%;
66; Conservation
                                               (TrEMBLrel. (TrEMBLrel. (TrEMBLrel.
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 (Human)
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RasGEFN; 1.
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РН; 2.
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                                               Created)
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Pred. No. 2.17e-38;
71; Mismatches 101;
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Ras-GRF2, a novel
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Mus.
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Search completed: Sat Apr 22 13:22:56 2000 Job time : 128 secs.
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Best Local S
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TISSUB-BRAIN;
MEDLINE; 97349984.
NAGASE T., ISHIKAWA K., NAKAJIMA D., OHIRA M., SEKI N., MIYAJIMA N.,
PROBASE T., ISHIKAWA K., NAKAJIMA D., OHIRA M., SEKI N., MIYAJIMA N.,
PROBASE T., ISHIKAWA K., NAKAJIMA D., OHIRA M., SEKI N., MIYAJIMA N.,
PROBASE T., ISHIKAWA K., NAKAJIMA D., OHIRA M., SEKI N., MIYAJIMA N.,
PROBASE T., ISHIKAWA K., NAKAJIMA D., OHIRA M., SEKI N., MIYAJIMA N.,
PROBASE T., ISHIKAWA K., NAKAJIMA D., OHIRA M., SEKI N., MIYAJIMA N.,
PROBASE T., ISHIKAWA K., NAKAJIMA D., OHIRA M., SEKI N., MIYAJIMA N.,
PROBASE T., ISHIKAWA K., NAKAJIMA D., OHIRA M., SEKI N., MIYAJIMA N.,
PROBASE T., ISHIKAWA K., NAKAJIMA D., OHIRA M., SEKI N., MIYAJIMA N.,
PROBASE T., ISHIKAWA K., NAKAJIMA D., OHIRA M., SEKI N., MIYAJIMA N.,
PROBASE T., ISHIKAWA K., NAKAJIMA D., OHIRA M., SEKI N., MIYAJIMA N.,
PROBASE T., ISHIKAWA K., NAKAJIMA D., OHIRA M., SEKI N., MIYAJIMA N.,
PROBASE T., ISHIKAWA K., NAKAJIMA D., OHIRA M., SEKI N., MIYAJIMA N.,
PROBASE T., ISHIKAWA K., NAKAJIMA D., OHIRA M., SEKI N., MIYAJIMA N.,
PROBASE T., ISHIKAWA K., NAKAJIMA D., OHIRA M., SEKI N., MIYAJIMA N.,
PROBASE T., ISHIKAWA K., NAKAJIMA D., OHIRA M., SEKI N., MIYAJIMA N.,
PROBASE T., ISHIKAWA T., NOMURA N., OHIRA M., SEKI N., MIYAJIMA N.,
PROBASE T., ISHIKAWA T., NOMURA N., OHIRA M., SEKI N., MIYAJIMA N.,
PROBASE T., ISHIKAWA T., NOMURA N., OHIRA M., SEKI N., MIYAJIMA N.,
PROBASE T., ISHIKAWA T., NOMURA N., OHIRA M., SEKI N., MIYAJIMA N.,
PROBASE T., ISHIKAWA T., NOMURA N., OHIRA M., SEKI N., MIYAJIMA N.,
PROBASE T., ISHIKAWA T., NOMURA N., OHIRA M., SEKI N., MIYAJIMA N.,
PROBASE T., ISHIKAWA T., NOMURA N., OHIRA M., SEKI N., MIYAJIMA N.,
PROBASE T., ISHIKAWA T., NOMURA T., NOMURA T., NOMURA T., NOMURA T., NOMURA T.,
PRAMI T., NOMURA T., N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Local Similarity 25.8%;
hes 64; Conservative
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                                                                                                                                     QMSHRLEP 846
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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Sat Apr 22 13:19:37 2000; MasPar time 50.95 Seconds 497.627 Million cell updates/sec

Tabular output not generated.

Title: >US-09-422-999-18 (1-849) from US09422999.pep 6222

Description: Perfect Score: Sequence: 1 MVLWKRALTMTGFLTRRTHL.....VIDNQRTLSQMSHRLEPRRP 849

Scoring table: PAM 150 Gap 11

Searched: 82229 seqs, 29864866 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: swiss-prot38 1:swissprot

Statistics: Mean 55.453; Variance 99.565; scale 0.557

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

1 3 3 4 4 4 7 6 6 7 7 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	Result
1922 317 317 291 278 278 255 255 255 253 255 251 240 210 200 200 200 200 200 200 200 200 20	Score
0.000000000000000000000000000000000000	Query Match I
1213 1244 1264 1264 911 1333 1333 1589 1595 1253 377 376 1435 377 378 378 377 378 378 378 378 378 378	Length 1
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YNX5_CAEEL CC25_SACKL GNRP_RAT GNRP_MOUSE SSTE6_SCHPO SOS2_HUMAN SOS2_MOUSE SOS1_HOMAN CC25_CANAL CC25_YEAST YEAST KAPR_APLCA LTE1_YEAST KAPR_SCHPO KAPR_YEAST KAP1_HUMAN BUD5_YEAST	ID
HYPOTHETICAL 139.4 KD CELL DIVISION CONTROL GUANINE NUCLECTIDE REL GUANINE NUCLECTIDE REL GUANINE NUCLECTIDE REL STE6 PROTEIN. SON OF SEVENLESS PROTE SON OF SEVENLESS PROTE SON OF SEVENLESS PROTE SON OF SEVENLESS PROTE CELL DIVISION CONTROL CELL DIVISION CONTROL CELL DIVISION CONTROL CELL DIVISION PROTEIN. CAMP-DEPENDENT PROTEIN CAMP-DEPENDEN	Description
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45	44	43	42	41	40	39	38	37	36	35	34	33	32	34	30	29	28	27	26	25	24
143	151	153	157	159	162	165	165	166	166	165	166	165	165	171	172	173	177	181	180	180	184
2.3	2.4	2.5	2.5	2.6	2.6	2.7	2.7	2.7	2.7	2.7	2.7	2.7		2.7							
852	400	404	400	412	403	1584	762	762	762	417	417	415	403	385	379	369	327	381	380	379	390
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GNDS_MOUSE	KAP2_MOUSE	KAPR_COLTR	KAP2_BOVIN	KAPR_EMENI	KAP2_HUMAN	YJ9G_YEAST	KGP2_HUMAN	KGP2_MOUSE	KGP2_RAT	KAP3_BOVIN	KAP3_HUMAN	KAP3_RAT	KAPR_BLAEM	KAPR_NEUCR	KAPO_PIG	KAPR_STRPU	KAPR_DICDI	KAPO_HUMAN	KAPO_RAT	KAPO_BOVIN	KAPR_MAGGR
Ĥ	CAMP-DEPENDENT PROTEIN	HYPOTHETICAL 182.0 KD	CGMP-DEPENDENT PROTEIN	CGMP-DEPENDENT PROTEIN	CGMP-DEPENDENT PROTEIN	CAMP-DEPENDENT PROTEIN	CAMP-DEPENDENT PROTEIN	CAMP-DEPENDENT PROTEIN	CAMP-DEPENDENT PROTEIN	CAMP-DEPENDENT PROTEIN	CAMP-DEPENDENT PROTEIN	CAMP-DEPENDENT PROTEIN									
	N 7.03e-07	N 3.39e-07	N 7.81e-08	N 3.72e-08	N 1.21e-08	3.91e-09	N 3.91e-09	_	2.	N 3.91e-09	N 2.68e-09	N 3.91e-09	N 3.91e-09	N 3.96e-10	N 2.69e-10	_	N 3.87e-11	_	N 1.19e-11	N 1.19e-11	N 2.46e-12

ALIGNMENTS

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474 SRIQMSAIWQVLLNNGLISHIDGEHQFLDKINSYYRWVQQFRSRNKVAPSIEEV 527	414 EKQIRDSGGILHRKMLTDNHQVIRDITTEHTRVQNCMIGAEMIDWLLTLFVSTSTTCSSL 473 : : : : : : : :	Query Match 30.9%; Score 1922; DB 1; Length 1213; Best Local Similarity 38.5%; Pred. No. 0.00e+00; Matches 311; Conservative 204; Mismatches 259; Indels 33; Gaps 24;	SEQUENCE 1213 AA; 139379 MW; DB4E0F1E CRC32;	Fram; Provoto; masGern; I.	PF00617; RasGEF; 1	PFAM; PF00027; cNMP_binding; 2. PFAM; PF000610; DEP; 1.	PROSITE; PS50042; CNMP_BINDING_3; 2.	WORMDED: TSOOG 5: OFFICATO	PIR; S42368; S42368.	EMBL; Z30423; CAA83013.1;		or send an email to license@isb-shich)	license	as its content is in no	the European Bioinformatics Institute. There are no restrictions on its	between the Swiss Institute of Bioinformatics and the EMBL outstation	This SWISS-PROT entry is copyright. It is produced through a collaboration	SIMILARALLI IV CAME DEFENDENT FOUNDATION STRUCTURE CONTRACTOR CONT	mitted (MAR-1994) to	BERKS M., SMITH A.;	STRAIN=BRISTOL N2;	SEQUENCE FROM N.A.	Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.	Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;	Caenorhabditis elegans.	T2005.5	Rel. 32, Last annotation update)	(Rel. 28,	01-FEB-1994 (Rel. 28, Created)	YNS5_CAEEL STANDARD; PRT; 1213 AA.	

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                      SEQUENCE FROM N.A.

MEDLINE; 92354938.

PRIGOZY T., GONZALES E., BROEK
"Identification and analysis of
kluyveri that can complement the
Saccharomyces cerevisiae.";
Gene 117:67-72(1992).
                                                                                                                                                                              002342;
01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last seguence update)
15-JUL-1999 (Rel. 38, Last annotation update)
CELL DIVISION CONTROL PROTEIN 25 (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                       1181
                                                                                                                                                 Saccharomyces kluyveri (Yeast)
Eukaryota; Fungi; Ascomycota;
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 FUNCTION: PROMOTES THE PROTEIN POSITIVELY CONT
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THE EXCHANGE CONTROLS THE
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OF RAS-BOUND GDP BY GTP. 1
LEVEL OF CELLULAR CAMP AT
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of CDC25
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Best Local S
Matches
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01-DEC-1992
01-DEC-1992
15-JUL-1999
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                                                                                                                                                         "Molecular cloning of cDN factor for Ras p21.";
Nature 358:351-354(1992).
                                                                                                                                                                                                                                                                      Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata;
Eutheria; Rodentia; Sciurognathi; Murid
                                                                                                                                                                                                                                                                                                                    GUANINE NUCLEOTIDE RASGRF1.
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                                                                                                  -I- FUNCTION: PROMOTES THE EXCHANGE OF RAS-BOUND
-I- SIMILARITY: CONTAINS 1 DBL-HOMOLOGY DOMAIN (I
-I- SIMILARITY: CONTAINS 2 PH DOMAINS.
-I- SIMILARITY: CONTAINS 1 RASGEF DOMAIN.
                                                                                                                                                                                                                  MEDLINE;
                                                                                                                                                                                                       SHOU C., FARUSWORTH C.
                                                                                                                                                                                                                                   TISSUE=BRAIN;
                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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PF00618; RasGEFN;
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non-profit institutions as long and this statement is not removed requires a license agreement (See
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24, Last sequences 38, Last annotations
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                                                                                                                                                                                     .L., NEEL B.G., FEIG L.A.;
cDNAs encoding a guanine-nucleotide-releasing
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Pred. No. 1.63e-37;
50; Mismatches 81
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Rattus.
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P27671;
Ol-AUG-1992 (Rel. 23, Created)
Ol-OCT-1996 (Rel. 34, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
GUANINE NUCLEOTIDE RELEASING PROTEIN (GNRP).
RASGRE1 OR CDC25MM OR GRE1.
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MARTEGANI E., VANONI M., ZIPPEL R., COCCETTI P., BRAMBILLA R., FERRARI C., STURANI E.P., ALBERGHINA L.; "Cloning by functional complementation of a mouse cDNA encoding homologue of CDC25, a Saccharomyces cerevisiae RAS activator."; EMBO J. 11:2151-2157(1992).
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DOMAIN
                                                                                                                                SEQUENCE OF 791-1262 FROM N.A. STRAIN-SWISS; TISSUE-BRAIN; MEDLINE; 92289680.
                                                                                                                                                                                                                       "Isolation of multiple mouse cDNAs with coding Saccharomyces cerevisiae CDC25: identification Bcr, Vav, Dbl and CDC24."; EMBO J. 11:4007-4015(1992).
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (Mouse).
Musculus (Mouse).
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PF00618;
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PS00741; GDS_CDC24;
PS50003; PH_DOMAIN;
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RhoGEF; 1.
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74; Mismatches
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STE6 PROTEIN
                                                                                                                                                                                                                                                                                                                                                                       CONFLICT
SEQUENCE
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PROSITE;
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PFAM; PFC
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"Identification of a mammalian gene structurally and fun-
related to the CDC25 gene of Saccharomyces cerevisiae.";
Proc. Natl. Acad. Sci. U.S.A. 89:7100-7104(1992).
-!- FUNCTION: PROMOTES THE EXCHANGE OF RAS-BOUND GDP BY
-!- TISSUE SPECIFICITY: BRAIN.
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PFAM;
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Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Archiascomycetes;
Schizosaccharomycetales; Schizosaccharomycetace
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PFAM; PF00621; Rhogef; 1.
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MGD; MGI:99694; RASGRF1.
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SIMILARITY: CONTAINS 1 DBL-HOMOLOGY DOMAIN (DH).
SIMILARITY: CONTAINS 1 RASGEF DOMAIN.
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PS00741; GDS_CDC24;
PS50003; PH_DOMAIN;
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                              MEDLINE; 93262494
CHARDIN P., CAMON
                                                                                                                                 ON ...
30S2.
Homo sapiens (Human).
Homo sapiens (Human).
Thervota; Metazoa; Chordata; Cr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the European Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
     BAR-SAGI D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PIR; S28098; S28098.
PROSITE; PS00720; GDS_CDC25;
PROSITE; PS50002; SH3; 1.
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-i- SIMILARITY: CONTAINS 1 S43 DOMAIN.
-i- SIMILARITY: CONTAINS 1 RASGEF DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HUGHES D.A., FUKUI Y., YAMAMOT "Homologous activators of ras Nature 344:355-357(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
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[1]
                                                                                     TISSUE-BRAIN;
                                                                                                           SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Match 4.5%;
Local Similarity 22.2%;
les 57; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RSYVRQLNVIDNQRTLS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIISALNSSPIHRLRKTWANLNSKTLASFELLNNLTEARKNFSNYRDCLENCVLPCVPFL 814
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -FKKTTANLDLFLRRFNEIQFWVVTEICLCSQLSKRVQLLKKFIKIAAHCKEYKNLNSFF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QELEDLS-LHNSPDPIIYKDELVLLLPPREIAKQLCILEFQSFSHISRIQFLTKIWDNLN 696
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GVYFTDLTELKTGNKDNFQNMINFDKRTKVTRILNEIKKFQSVGYMFNPINEVQELLNEV
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90190870.
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                                 CAMONIS J.H.,
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                                 GALE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 278;
Pred. No. 9
75; Mismat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  factor; SH3 domain SH3.
                                                                                                                                                               Craniata; Vertebrata; i; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ij
                              N.W.,
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                           VAN AELST L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3; DB 1;
9.01e-30;
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                              WIGLER M.
                                                                                                                                                                                           Mammalia;
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PFAM;
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                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS00720; GDS_CDC25; PROSITE; PS50003; PH_DOMAIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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-1- SIMILARITY: CONTAINS 1 PH DOMAIN.
-1- SIMILARITY: CONTAINS 1 RASGEF DOMAIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE-PLACENTA;
                                                                                                                                                                                                                             SEQUENCE
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[2]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 724-1296 FROM N.A.
 763
                      929
                                             704
                                                                                                                                                         752 FESPPPPIEWHISKPGQFETFDLMTLDPIEIARQLTLLESDLYRKVQPSELVGSVWTKED
PLLIKDMTFTHEGNKTFI---D-NLVNFEKMRMIANTARTVRYYRSQPF
                                                        IVSAVNSVSYYRLDHTFEALQERKRKIL-D-EA-VELSQDHFKKYLVKLKSINPPCVPFF
                      GIYLTNILKTEEGNNDFLKRKGKDLINFSKRRKVAEITGEIQQYQNQPY
                                           IVMGLSNIAVSRLALTWEKLPSKFKKFYAEFESLMDPSRNH-RAYRLTVAKLEPPLIPFM
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                                                                                         FKKTTANLDLFLRRFNEIQFWVVTEICLCSQLSKRVQLLKKFIKIAAHCKEYKNLNSFFA
                                                                                                             KEINSPHLLKMIRHTTHLTLWFEKCIVEAENFEERVAVLSRIIEILQVFQDLHNFNGVLE 871
                                                                                                                                     FDSLTPLPEQEGPTVGTVGTFELMS--SKDLAYQMTIYDWELFNCVHELELIYHTFGRHN
                                                                                                                                                                                                                                                                                                                                                                                                                      PF00618; RasGEFN; PF00621; RhoGEF; 1
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ilarity 25.8%;
Conservative
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AAA91852.1;
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Q -> R (IN REF. 2).
R -> K (IN REF. 2).
S -> C (IN REF. 2).
S -> E (IN REF. 2).
T -> A (IN REF. 2).
CGS -> LC (IN REF. 2).
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                                                                                                                                                                                          Score 272; DB 1;
Pred. No. 1.33e-28;
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Q -> E
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POLY-PRO.
POLY-PRO.
POLY-PRO.
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                                                                                                                                                                                                                             CRC32;
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15-JUL-1999
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 SOS1_MOUSE
Q62245; Q62244;
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DOMAIN
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PFAM; PF00617; Rasi
PFAM; PF00618; Rasi
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MGD; MGI:98355; SOS2.
PROSITE; PS00720; GDS_CDC25;
PROSITE; PS50003; PH_DOMAIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BOWTELL D.D., FU P., SIMON M.A., SENIOR P.V.;
"Identification of murine homologues of the Drosophila sevenless gene: potential activators of ras.";
Proc. Natl. Acad. Sci. U.S.A. 89:6511-6515(1992).
-!- FUNCTION: PROMOTES THE EXCHANGE OF RAS-BOUND GDP BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -1- TISSUE SPEĆIFICITY: EXPRESSED IN MOST EMERYONIC AND -1- SIMILARITY: CONTAINS 1 DBL-HOMCLOGY DOMAIN (DH).
-1- SIMILARITY: CONTAINS 1 PH DOMAIN.
-1- SIMILARITY: CONTAINS 1 RASGEF DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN-SWISS; TISSUE-EYE;
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                                                                                                                                                                                                                                                                                                                                                                                           Guanine-nucleotide releasing
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                                                                                                                                                                                                                                                                                                                     DOMAIN
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                                                                                                                                                                                                                               FESSPPPVEWHISRTGOFETFDLMTLHPIEIARQLTLLESDLYRKVQPSELVGSVWTKED 776
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the EN
                                                                                   GIYLTNILKTEEGNSDFLKRKGKDLINFSKRRKVAEITGEIQQYQNQPY
                                                                                                        FKKTTANLDLFLRRENEIQFWVVTEICLCSQLSKRVQLLKKFIKIAAHCKEYKNLNSFFA
                                                                                                                                                                               KEINSPNLLKMIRHTINLTLWFEKCIVEAENFEERVAVLSRIVEILQVFQDLNNFNGVLE
                                                            PLLIKDMTFTHEGNKTFI---D-NLVNFEKMRMIANTARTVRYYRSQPF
                                                                                                                                                                                                         FDSLTPLPEQEGPTVGTVGTFELMS--SKDLAYQMTIYDWELFNCVHELELIYHTFGRHN 643
                                                                                                                                                                                                                                                                                                                                                                                                         PF00621;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Z11664; CAA77732.1; -.
                                                                                                                                                                                                                                                                    Similarity
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Rodentia;
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(Rel.
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larity 24.9%;
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             STANDARD;
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. 38, Last sequence update)
. 38, Last annotation update)
PROTEIN HOMOLOG 2 (SOS-2) (MSOS-2) (FRAGMENT).
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                                                                                                                                                                                                                                                                                                      148846 MW; 13A2E0E3 CRC32;
                                                                                                                                                                                                                                                      Score 266;
Pred. No. 1.
70; Mismatc
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PH.
RASGEF.
POLY-PRO.
POLY-PRO.
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             PRT;
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.95e-27
             AA
                                                                                                                                                                                                                                                         92;
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15-JUL-1999 (Rel. 38, 1
15-JUL-1999 (Rel. 38, 1
SON OF SEVENLESS PROTEJ
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DOMAIN
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J. Mol. Biol. 269:579-591(1997).
-i- FUNCTION: PROMOTES THE EXCHANGE OF RAS-BOUND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Guanine-nucleotide releasing DOMAIN 202 443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PFAM; PF00169; PH; 1. PFAM; PF00617; RasGEF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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-i- TISSUE SPECIFICITY: EXPRESSED IN MOST EMBRY
-i- SIMILARITY: CONTAINS 1 DBL-HOMOLOGY DOMAIN
-i- SIMILARITY: CONTAINS 1 PH DOMAIN.
-i- SIMILARITY: CONTAINS 1 RASGEF DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BOWTELL D., FU P., SIMON M., SENIOR P., Identification of murine homologues of the Drosophila sevenless gene: potential activators of ras.", Proc. Natl. Acad. Sci. U.S.A. 89:6511-6515(1992).
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STRAIN-SWISS; TISSUE-EYE;
MEDLINE; 92335328.
                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota;
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FDSLTPLPEQEGPTVGTVGTFELMS--SKDLAYQMTIYDWELFNCVHELELIYHTFGRHN
                                                                                                                                                                                                                                                                                            FQSSPPTVEWHISRPGHIETFDLLTLHPIEIARQLTLLESDLYRAVQPSELVGSVWTKED
                                                                                               VVSAMNSSPYYRLDHTFEQIPSRQKKILEEAHELSE-DHYKK-YLAKLRSINPPCVPFFG
                                                                                                                                                              FKKTTANLDLFLRRFNEIQFWVVTEICLCSQLSKRVQLLKKFIKIAAHCKEYKNLNSFFA
                                                                                                                                                                                                           KEINSPNLLKMIRHTTNLTLWFEKCIVETENLEERVAVVSRIIEILQVFQELNNFNGVLE
                                                                       IVMGLSNIAVSRLALTWEKLPSKFKKFYAEFESLMDPSRNHRAYRLTVAKLEPPLIPFMP
                                                                                                                                                                                                                                                                                                                                                                    4.18;
Similarity 25.48;
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Etazoa; Chordata; Craniata; Vertebrata;
Mentia; Sciurognathi; Muridae; Murinae;
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Last annotation updat
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Pred. No. 2.
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2.55e-25;
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                                                   SEQUENCE
                                                                                                                                                                              PROSITE; PROSITE;
                                                                                                                                                                                                                                                                                      use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for contentitles requires a license.
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                                                                                                                                                                                                                                                                                                                                                                                                                                   "Crystal structure of the Dbl and pleckstrin homology domains the human Son of sevenless protein."; Cell 95:259-268(1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "The solution structure of the pleckstrin homology domain of human SOS1. A possible structural role for the sequential association of diffuse B cell lymphoma and pleckstrin homology domains."; J. Biol. Chem. 272:30340-30344(1997).
                                                                                                                                                      PFAM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (Human).
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eukaryota; Metazoa; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SON OF SEVENLESS PROTEIN HOMOLOG 1 (SOS-1).
                                                                             DOMAIN
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                                                                                                                                                                                                                                                                                    entities
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         to GRB2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BAR-SAGI D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CHARDIN P., CAMONIS J.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE-BRAIN;
                                                                                                                 Guanine-nucleotide
                                                                                                                                          PFAM;
                                                                                                                                                                     PFAM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Science 260:1338-1343(1993).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EDLINE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Human Sosl: a guanine nucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS)
                                                                                                                                                                                                                                                                                                                                                                          SIMILARITY: CONTAINS 1 DBL-HOMOLOGY D
SIMILARITY: CONTAINS 1 PH DOMAIN.
SIMILARITY: CONTAINS 1 RASGEF DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                               FUNCTION: PROMOTES THE EXCHANGE OF RAS-BOUND GDP SUBUNIT: INTERACTS WITH GRB2.
                                                                                                                                                                                                           182530
                                                                                                                                                                                                                     1AWE; 25-FEB-98.
1DBH; 23-DEC-98.
                                                                                                                           PF00618; RasGEFN; 1
PF00621; RhoGEF; 1.
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PF00617; RasGEF; 1.
                                                                                                                                                                                                                                              L13857; AAA35913.1;
 Similarity
58; Conser
                                                                                                                                                                             PS00720; GDS_CDC25; PS50003; PH_DOMAIN;
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larity 25.48;
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Score 257; DB 1; In Pred. No. 1.06e-25; 65; Mismatches 97;
                                                             RASGEF.
POLY-PRO.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CELL DIVISION (
CDC25 OR CSC25
                                                                     1071 ELARQLTLREFKLY-CKITKFACLAKVWGKKSGLSESIDSITQFIKASNQLTNFVGYMI- 1128
                                                                                                                                                                                      Mitosis; SH3 domain.
                                                                                                                                                                                                       Guanine-nucleotide releasing
                                                                                                                                                                                                                   PFAM; PF00018; SH3; 1.
PFAM; PF00617; RasGEF; 1.
PFAM; PF00618; RasGEFN; 1
                                                                                                                                                                                                                                 PROSITE; PS00720; GDS_CDC25; PROSITE; PS50002; SH3; 1. PFAM; PF00018; SH3; 1. PFAM; PF00617; RasGEF; 1.
                                                                                                                                                                                                                                                                                            EMBL;
                                                                                                                                                                                                                                                                                                                                      entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EUR. J. BIOChem. 213:195-204(1993).
11- FUNCTION: PROMOTES THE EXCHANGE OF RAS-BOUND GDP BY GTP. THIS PROTEIN POSITIVELY CONTROLS THE LEVEL OF CELLULAR CAMP AT START, THE STAGE AT WHICH THE YEAST CELL DIVISION CYCLE IS TRIGGERED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "A Candida albicans homolog cerevisiae.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=792-1
MEDLINE; 932
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Candida albicans (Yeast).
Eukaryota; Fungi; Ascomyo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P43069;
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                                                                                                                                                             SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Candidaceae; Candida.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15-JUL-1999
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                                                                                                                                                                          DOMAIN
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LRKADPKKRVQIIRYFIQVADKCRQYNNFSSMTAIISALYSSPIHRLKKTWEYMNADALS 1188
                                          DLAYQMTIYDWELFNC-VHELELIYHTFGRHN-FKKTTANLDLFLRRFNEIQFWVVTEIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IYLTNILKTEEGNPEVLKRHGKELINFSKRRKVAEITGEIQQYQNQPY
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                                                                                                                                                                                                                                                                                            M94160; CAB26565.1; .. P29354; 1GFD.
                                                                                                                 Similarity
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                                                                                                                                                           30
1333 AA;
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                                                                                                   Conservative
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Rel. 38, Last annotation
CONTROL PROTEIN 25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ascomycota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              32, Created)
32, Last seq
                                                                                                               4.1%;
                                                                                                                                                           94 SH3.
152012 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GROSS
                                                                                               Score 253; DB 1;
Pred. No. 6.15e-25;
60; Mismatches 87
                                                                                                                                                                                                       factor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hemiascomycetes; Saccharomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        E., LEVITZKI A., SIMCHEN CDC25 is functional in Sa
                                                                                                                                                             062F32ED CRC32;
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                                                                                                                                                                                                       Cell division;
                                                                                                                                                                                                                                                                                                                                                    (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 update)
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                                                                                                   87;
                                                                                                                              Length 1333;
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CC25_YEAST
P04821;
                                                                                                                                                                                                                                             JOHNSTON M., ANDREWS S., BRINKMAN R., COOPER J., DING H., DI FAVELLO A., FULTON L., GATTUNG S., GRECO T., KIRSTEN J., KUCABA T., HALLSWORTH K., HAWKINS J., HILLIER L., JIER M., JOHNSON D., JOHNSTON L., LANGSTON Y., LARREILLE P., LE T., JOHNSON E., MENEZES S., MILLER N., HANN M., PAULEY A., PELUSCRIFKEN L., RILES L., TAICH A., TREVASKIS E., VIGNATI D., WATERSTON R., WATERSTON R.; Submitted (NOV-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13-AUG-1987 (Rel. 05, Created)
01-JAN-1988 (Rel. 06, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
CELL DIVISION CONTROL PROTEIN 25.
CDC25 OR CTN1 OR YLR310C OR L2142.6.
Saccharomyces cerevisiae (Baker's yeast).
                      This SWI
                                              JONES S., VIGNAIS M.L., BROACH J.R.;
"The CDC25 protein of Saccharomyces cerevisiae promotes exchange of guanine nucleotides bound to ras.";
MO1. Cell Biol. 11:2641-2646(1991).
-!- FUNCTION: PROMOTES THE EXCHANGE OF RAS-BOUND GDP BY GTP. THIS PROTEIN POSITIVELY CONTROLS THE LEVEL OF CELLULAR CAMP AT START, THE STAGE AT WHICH THE YEAST CELL DIVISION CYCLE IS TRIGGERED.
-!- SIMILARITY: CONTAINS 1 RASGEF DOMAIN.
                                                                                                                                                                                                                                                                                                                                                               "Characterization, cloning and sequence analysis of the CDC25 which controls the cyclic AMP level of Saccharomyces cerevisian BO J. 5:375-380(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                             "The S. cerevisiae CDC25 cyclase pathway."; Cell 48:789-799(1987).
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POWERS S., WIGLER M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1248
                                                                                                                                                                                                        DOMAINS.
MEDLINE; 89181526.
MUNDER T., MINK M.
                                                                                                                                                                                                                                                                                                                                  STRAIN-S288C
                                                                                                                                                                                                                                                                                                                                                                                                       CAMONIS J.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. MEDLINE; 86220116.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. MEDLINE; 87131091.
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                                                                                                                                            MEDLINE; 91203884.
                                                                                                                                                         FUNCTION
                                                                                                                                                                                       mitosis
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                                                                                                                                                                                                                                                                                                                                                                                              JACQUET M.
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 SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the EMEUROPEAN BIOINFORMATICS. There are no restrictly non-profit institutions as long as its content
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                                                                                                                                                                                   T., MINK M., KUNTZEL H.;
s of the Saccharomyces cerevisiae
and melosis.";
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                                                                                                                                                                           214:271-277(1988).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  product
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              Jh a collaboration
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                              collaboration
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Query Match
Best Local
SEQUENCE FROM N.A. MEDLINE; 92034991. SIMON M.A., BOWTELL "Ras1 and a putativ
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TRANSMEM
                                                                                                                                                                                                                                                                                                                                      SOS_DROME
P26675;
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PROSITE; PS00720; GDS_CDC25;
PROSITE; PS50002; SH3; 1.
PFAM; PF00018; SH3; 1.
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                                                                           BONFINI L., KARLOVICH C.A., "The Son of sevenless gene | Science 255:603-606(1992).
                                                                                                                                                                                         Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; MuscEphydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                        01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last sequence up
15-JUL-1999 (Rel. 38, Last annotation
SON OF SEVENLESS PROTEIN.
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                                                                                                                                            SEQUENCE FROM N.A.
STRAIN=OREGON-R;
                                                                                                                          MEDLINE; 92141820.
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PF00618;
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U17247;
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1452 1473
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497
954
1589
BOWTELL D.D.L., DODSON putative guanine nucleo
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AAA34478.1;
AAB67360.1;
AAB64528.1;
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nucleotide
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No. 2.55e-25
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p14771;
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01-FEB-1996 (Rel. 33, Last seque
15-JUL-1999 (Rel. 38, Last annot
SCD25 PROTEIN.
SCD25 OR SDC25 OR YLL016W.
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IS SUBUNIT: MAY FORM A COMPLEX WITH SEVENLESS
I- SIMILARITY: CONTAINS 1 DBL-HOMOLOGY DOMAIN
I- SIMILARITY: CONTAINS 1 PH DOMAIN.
I- SIMILARITY: CONTAINS 1 RASGEF DOMAIN.
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                                                           SCD25 OR SDC25 OR YLL016W.
Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Hemiascomycetes;
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CRECHET J.B., POULLET P., MISTOU M.-Y., BOY-MARCOTTE E., DAMAK F., JACQUET M.;
"Enhancement of the GDP-GTP exchange of terminal domain of SCD25.";
Science 248:866-868(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BOY-MARCOTTE E., DAMAK F., CAMONIS J., GARREAU H., JACQUET THE C-terminal part of a gene partially homologous to CDC suppresses the cdc25-5 mutation in Saccharomyces cerevisiae Gene 77:21-30(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DAMAK F., BOY-MARCOTTE E., LE ROSCOUET D., GUILBAUD R., JA "SDC25, a CDC25-like gene which contains a RAS-activating is a dispensable gene of Saccharomyces cerevisiae."; mol. Cell. Biol. 11:202-212(1991).
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DAMAK F., BOY-MAR
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                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -i- MISCELLANEOUS: SUPPRESSES THE CDC25-5
CAMP LEVEL) AND HAS SIMILAR FUNCTIONS
-i- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
-i- SIMILARITY: CONTAINS 1 RASGEF DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REY I., SCHWEIGHOFFER F., BARLAT I., CAMONIS J., BOY-GUILBAUD R., JACQUET M., TOCQUE B.;

"The COOH-domain of the product of the Saccharomyces

gene elicits activation of p21-ras proteins in mammal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE;
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PFAM; PF00617; RasGEF; 1.
PFAM; PF00618; RasGEFN; 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Oncogene 6:347-349(1991).
-I- FUNCTION: PROMOTES THE EXCHANGE OF RAS-BOUND GDP
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                                                                                                                                                                                DOMAIN
VARIANT
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PIR; S14177; S
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                                                                                                                                                                                                                                                                                                           PROSITE; PS00720; GDS_CDC25; PROSITE; PS50002; SH3; 1.
                                                      676
                                                                                                                                                                                                                                         domain
                            KLMDPKKNFINYRNELKSLHSAPCVPFFGVYLSDLTFTDSGNPDYL 1126
                                                     SKRVQLLKKFIKIAAHCKEYKNLNSFFAIVMGLSNIAVSRLALTWEKLPSKFKKFYAEFE
                                                                                                                                                                                                                                                                                                                                       L0002822;
SLMDPSRNHRAYRLTVAKLEP-PLIPFMPLLIKDMTFTHEGNKTFI
                                                                                                              Similarity 36; Conse
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larity 34.0%;
Conservative
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                                                                                                                                                                     144979
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                                                                                                             Score 240; DB 1;
Pred. No. 1.80e-22;
26; Mismatches 43
                                                                                                                                                                   SH3.
POLY-ASN.
POLY-ARG.
DVVVKFI -> V
MW; 36110264
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                                                                                                                                                                                                                                                       factor;
                                                                                                                                                                                                                                                         cell
                                                                                                                                                                                                                                                                                                                                                                                                         (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RAS proteins by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PARMEGGIANI A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MUTATION IN YEAST AS CDC25.
                                                                                                                                                                     (IN STRAIN OL136)
CRC32;
                                                                                                                                                                                                                                                         cycle;
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                                                                                                                                          Length 1253;
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REPEAT
                                                                                                                                                                             SEQUENCE
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PROSITE; PS00888; CNMP_BINDING_1;

PROSITE; PS00889; CNMP_BINDING_2;

PROSITE; PS50042; CNMP_BINDING_3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ď
                                                                                                                                                                                                                                                                                                REPEAT
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BERGOLD P.J., BEUSHAUSEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JUL-1993 (Rel.
01-JUL-1993 (Rel.
15-DEC-1999 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KAPR_APLCA
P31319;
     192
                                       195
                                                           134 FSHLDDNERSDIFDAM-FPVHRHAGEVIIQQGDEGDNEYVIDQGEVDVYV-NNVHVTSIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  between
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sensitization."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "A regulatory subunit of the cAMP-dependent protein kinase down-
regulated in aplysia sensory neurons during long-term
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SCHWARTZ J.H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Aplysiidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Aplysia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KINASE A).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CAMP-DEPENDENT PROTEIN KINASE
                                                                                                                       Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      e by non-profit institutions as long dified and this statement is not removed. titles requires a license agreement (See send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CON 8:387-397(1992).

SUBUNIT: THE INACTIVE FORM OF THE ENZYME IS CHECKLATORY CHAINS AND TWO CATALYTIC CHAINS. A PRODUCES TWO ACTIVE CATALYTIC MONOMERS AND A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY:
SIMILARITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PTM: THE PSEUDOPHOSPHORYLATION SITE BINDS BINDING REGION OF THE CATALYTIC CHAIN BUT THE PHYSIOLOGICAL SIGNIFICANCE OF PHOSPHORE OF PHOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       JH0590; OKGAR1.
EGGSFGELALIYGTPRAATVKAKTDV-KLWGIDRDSYRRIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KINASES IS UNCLEAR.
                              LSHLSTTVKRELAGVLIFESHAKGGTVLFNQGEEGTSWYIILKGSVNVVIYGKGVVCTLH 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SWISS-PROT entry is copyright. It is produced through
een the Swiss Institute of Bioinformatics and the E
                                                                                                                                                                                                                                                                                                                                                                                                                                    PF00027; cNMP_binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HAT BINDS FOUR CAMP MOLECULES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        X62382; CAA44246.1;
                                                                                                        Similarity 33; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   californica
                                                                                                     3.5%;
larity 32.7%;
Conservative
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133
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                                                                                                                                                                                                                                                                                                                                                                                                                  Phosphorylation; Repeat;
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39,
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              S.A.,
                                                                                                   Score 216;
Pred. No. 5.
26; Mismatc
                                                                                                                                                                                                                            CAMP.
                                                                                                                                                                                                                                        ACETYLATION (BY PHOSPHORYLATION CAMP.
                                                                                                                                                                                                                                                                                                                               CAMP.
                                                                                                                                                                                                            CAMP.
                                                                                                                                                                                         CAMP
                                                                                                                                                                                                                                                                                                                                                   CAMP
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                                                                                                                                                                                                                                                                                                                                                                                DIMERIZATION AND PHOSPHORYLATION
                                                                                                                                                                                                                                                                                                                                                                                                  BY SIMILARITY
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                                                                                                                                                                                                                                                                                                                                                                                                                Acetylation.
                                                                                                                   DB 1;
.09e-18;
                                                                                                                                                                       CRC32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       http://www.isb-sib.ch/announce/
                                                                                                     39;
                                                                                                                                                                                                                                                          (BY
                                                                                                                                                                                                                                                                             SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Usage
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IS NOT PHOSPHORYLATED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         its content
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                                                                                                                                   Length
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                                                                                                                                                                                                                                                         SIMILARITY).
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                                                                                                                                                    DISULFID
                                                                                                                                                                                                                                                                                                                                                              WORMPEP;
PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fo entitles requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                                                                                   DISULFID
                                                                                                                                                                                                                                                                    CAMP-binding;
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; J05220; AAA27980.1; -.
EMBL; U39652; AAA80405.1; -.
PIR; A35076; OKKWIR.
HSSP; P00514; 1APK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-BRISTOL N2;
MEDLINE; 90153982.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KIN-2 OR KIN-A OR R07E4.6.
Caenorhabditis elegans.
Eukaryota; Metazoa; Nematc
                                                                                                                                                                            REPEAT
                                                                                                                                                                                            REPEAT
                                                                                                                                                                                                                                                                                                         PFAM; PF00027;
                                                                                                                                                                                                                                                                                                                             PROSITE;
                                                                                                                                                                                                                                                                                                                                               PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                elegans.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (NOV-1995) to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    regulatory subunit of cAMP-dependent protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Cloning, structure, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LU X.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      255
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KINASES IS UNCLEAR. SIMILARITY: CONTAINS SIMILARITY: BELONGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            nitted (NOV-1995) to the EMBL/GenBank/DDBJ databases. SUBUNIT: TETRAMER, COMPOSED OF 2 REGULATORY (R) AND (C) SUBUNITS. IN THE PRESENCE OF CAMP IT DISSOCIATES MONOMERIC C SUBUNITS AND AN R DIMER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PTM: THE PSEUDOPHOSPHORYLATION SITE BINDS TO THE BINDING REGION OF THE CATALYTIC CHAIN BUT IS NOT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           THE PHYSIOLOGICAL
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                                                                                                                                                                                                                                                                                                                       PS50042;
                                                                                                                                                                                                                                                                                                                                           PS00889;
                                                                                                                                                                                                                                                                                                                                                                                R07E4.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SS-PROT entry is copyright. It is produced through the Swiss Institute of Bioinformatics and the EN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chem.
                                                                                                                                                                                                                                                                                                                                                                PS00888;
     97
197
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Rhabditoidea; Rhabditidae; pel
                                                                                                                                                                                                                                                                                                     cNMP_binding;
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                                                                                                                                                                                                                                                                    hosphorylation;
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; CNMP_BINDING_2;
; CNMP_BINDING_3;
NMP_binding; 2.
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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Sat Apr 22 13:18:40 2000; MasPar time 36.15 Seconds 941.038 Million cell updates/sec

Tabular output not generated.

Title: >US-09-422-999-18 (1-849) from US09422999.pep 6222

Description: Perfect Score:

Sequence: 1 MVLWKRALTMTGFLTRRTHL.....VIDNQRTLSQMSHRLEPRRP 849

Scoring table: PAM 150 Gap 11

Searched: 122810 seqs, 40068593 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

pir62 1:pir1 2:pir2 3:pir3 4:pir4

Statistics: Mean 53.983; Variance 117.292; scale 0.460

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

23	າ 21 ວ່າ	20	19	18	17	16	15	14	13	12	11	10	9	8	7	ō	G	4	ω	2	~	Result
201	206	204	207	205	208	210	216	236	240	251	255	255	253	255	266	278	287	291	310	317	1922	Score
3.2	ຸພ	ω . ω	ω ω	3. ₃	ω 	3.4	3.5	3.8	3.9	4.0	4.1	4.1	4.1	4.1	4.3	4.5	4.6	4.7	5.0	5.1	30.9	Query Match
379	411	381	381	377	376	1435	378	1250	1048	1596	1589	1336	1333	1333	1297	911	1275	1260	1244	1095	1213	Length
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OKHUR1	S18634	OKMSR1	A60669	OKFF1R	OKKW1R	BVBYL1	OKGAR1	S14177	S64758	A41216	RGBYC5	S25716	S30356	A37488	S25714	S28098	A38985	S28407	S29083	PC1114	S42368	ID
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192 3.1 411 2 BY1368 probable cyclic nucle 191 3.1 538 1 BWBYD5 BUD5 protein - Yeast 180 2.9 379 1 OKBOIR protein kinase (EC 2. 181 2.9 381 1 OKHUIR protein kinase (EC 2. 180 2.9 381 1 OKDDRC 177 2.8 327 1 OKDDRC 178 2.8 434 2 S76944 hypothetical protein kinase (EC 2. 179 2.8 434 2 S76944 hypothetical protein kinase (EC 2. 170 2.8 434 2 S76944 hypothetical protein kinase (EC 2. 171 415 1 OKRUR2 protein kinase (EC 2. 172 416 1 OKHUR2 protein kinase (EC 2. 173 418 1 OKBOR2 protein kinase (EC 2. 174 418 1 OKBOR2 protein kinase (EC 2. 175 2.7 418 1 OKBOR2 protein kinase (EC 2. 175 2.7 418 1 OKBOR2 protein kinase (EC 2. 175 2.7 762 1 S46590 protein kinase (EC 2. 175 2.7 762 2 S68217 protein kinase (EC 2. 175 2.7 1584 2 S57161 hypothetical protein 162 2.6 244 2 C71347 probable catabolite gradien 162 2.6 404 1 OKBOZR protein kinase (EC 2. 151 2.4 401 1 OKBOZR protein kinase (EC 2. 151 2.4 401 1 OKBOZR protein kinase (EC 2. 151 2.4 401 1 OKBOZR protein kinase (EC 2. 152 2.5 400 1 OKBOZR protein kinase (EC 2. 153 2.4 401 1 OKBOZR protein kinase (EC 2. 154 2.4 1048 2 A70592 hypothetical protein	45	44	43	42	41	40	39	38	37	36	3 5	34	ω G	32	31	30	29	28	27	26	25	24
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probable cyclic BUD5 protein kinase	1048	401	400	404	224	1584	867	762	762	762	418	418	415	403	434	380	327	381	381	379	538	411
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ALIGNMENTS

KVEQYVHAGSVVFRQGEIGYYWYIYLKGAYEVNVNGK-IVCLLREGDDFGKLALVNDLPR 646	Db 588
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	Db 528
SRTQAVGMWQVLLEDGVLNHVDQEHHFQD-FYLFYRFLDDEHEDAPLPTEEEKKECDEEL 150	Qу 92
SRIOMS	Db 474
EKILR-AGKILRNAILSRAPHMIRDRKYHLKTYRQCCVGTELVDWMID-ETPCVH- 91	Qу 39
EKQIRDSGGILHRKMLTDNHQVIRDITTEHTRVQNC	Db 414
/ Match 30.9%; Score 1922; DB 2; Length 1213; Local Similarity 38.5%; Pred. No. 0.00e+00; nes 311; Conservative 204; Mismatches 259; Indels 33; Gaps 24;	Query Match Best Local (Matches 3)
nomology #label SOS #length 1213 #molecular-weight 139379 #checksum 3211	SUMMARY
domain CDC25-type guanine nucleotide exchange activator	987-1206
#d	FEATURE 574-689
<pre>domain homology; CDC25-type guanine nucleotide exchange activator homology</pre>	
# 5	CLASSIFICATION
ns 196/3; 238/1; 263/3; 312/3; 444/3; 519/3; 550/2; 669/2;	#introns
#cross-reterences EMBL:Z30423; NID:g458479; PID:g458480	0##
#residues 1-1213 ##label SMI	##1
le_type	##3
##status preliminary	#accession
ם	#submission
rs	#authors
S42368 S42368	REFERENCE
07-Aug-1998	
<pre>elegans #formal_name Caenorhabditis elegans 07-Oct-1994 #sequence revision 10-Nov-1995 #text change</pre>	ORGANISM DATE
1 S42368 #type complete guanine nucleotide releasing factor homolog - Caenorhabditis	RESULT ENTRY TITLE

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RESULT
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 Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                            Prigozy, T.; Gonzales, E.; Broek, D.
Gene (1992) 117:67-72
Identification and analysis of a DNA fragment from
Saccharomyces kluyveri that can complement the loss
CDC25 function in Saccharomyces cerevisiae.
                                                                                                                                                                                                                                                                                                                                                                   PC1114
PC1114
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SKCDC25 protein - yeast (Saccharomyces kluyveri) (fragme
#formal_name Saccharomyces kluyveri
30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change
09-Sep-1997
                                                                                                                                  #superfamily CDC25-type
homology
                                                                                                               transmembrane protein
                                                 #length
                                                             #domain CDC25-type guanine
homology #label SOS
                                                                                                                                                                                              1-1095 ##label PRI
:es GB:M82964; NID:g171186; PID:g171187
 5.1%;
32.5%;
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                                                 #checksum 2353
Score 317; DB 2;
Pred. No. 6.73e-31;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           #title Molecular cloning of cDNAs encoding a guanine-nucleotide-releasing factor #cross-references MUID:92350260 #accession $29083
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10-426
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                                                                           VNFEKMRMIANTARTVRYYRSQPFNPDAAQANKNHQDVRSYVRQLNVIDNQRTLSQMSHR
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                                                                                                                                                                                                                                 VTEICLCSQ-LSKRVQLLKKFIKIAAHCKEYKNLNSFFAIVMGLSNIAVSRLALTWEKLP
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                                                                                                                                                                                          KQTKSLFDKLQKLVSSDGRFKNLRETLRNCDPPCVPYLGMYLTDLAFLEEGTPNYTEDGL 1183
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#superfamily CDC25-type guanine nucleotide exchange activator
homology; CDC24 homology; pleckstrin repeat homology
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guanine-nucleotide-releasing protein -
CDC25 protein homolog
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Nature (1992) 358:351-354
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#domain CDC25-type guanine nucleotide exchange activator homology #label SOS
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Pred. No. 9.95e-30;
74; Mismatches 98
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#accession B46199
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#accession $22693
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##molecule_type nucleic acid
##residues 1029-1030, D', 1032-1224 ##label WEI
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Local Similarity 23.6%;
nes 49; Conservative
                                             VNFSKMRMISHIIREIRQFQQTTYKIDP 1227
                                                                                                                                                                                            VVTEICLCSQLSKRVQLLKKFIKIAAHCKEYKNLNSFFAIVMGLSNIAVSRLALTWEKLP 724
                                                                                                                                            KQTKSLLDKLQKLVSSDGRFKNLRESLRNCDPPCVPYLGMYLTDLVFIEEGTPNYTEDGL 1199
  VNFEKMRMIANTARTVRYYRSQPFNPDA 811
                                                                                              SKFKKFYAEFESLMDPSRNHRAYRLTVAKLEPPLIPFMPLLIKDMTFTHEGNKTFIDN-L 783
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Brambilla, R.; Ferrari, C.; Sturani, E.; Alberghina, L.
EMBO J. (1992) 11:2151-2157
Cloning by functional complementation of a mouse cDNA
encoding a homologue of CDC25, a Saccharomyces cerevisiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Wei, W.; Mosteller, R.D.; Sanyal, P.; Gonzales, E.; McKin. D.; Dasgupta, C.; Li, P.; Liu, B.X.; Brock, D. Proc. Natl. Acad. Sci. U.S.A. (1992) 89:7100-7104
Identification of a mammalian gene structurally and functionally related to the CDC25 gene of Saccharomyces
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homology; CDC24 homology; pleckstrin repeat homology
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       homology #label SôS
#length 1260 #molecular-weight 143900 #checksum 9725
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Pred. No. 1.40e-26;
63; Mismatches 93;
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                                                                                                                                                                                                      1146 LKKTWLKVSKQTKALIDKLQKLVSSEGRFKNLREALKNCDPPCVPYLGMYLTDLAFIEEG 1205
                                                                                                                                                                                                                                                                                             1086 KHFNDISNLIASEIIRNEDINARVSAIEKWVAVADICRCLHNYNAVLEITSSMNRSAIFR 1145
                                                                                                                                                           716
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[FICATION #superfamily CDC25-type guanine nucleotide exchange activator homology; CDC24 homology; pleckstrin repeat homology
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##residues 787-1275 ##label RES
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                                                                    NKTFIDN-LVNFEKMRMIANTARTVRYYRSQPFNPD
                                                                                                            TPNYTEDGLVNFSKMRMISHIIREIRQFQQTAYKIE 1241
                                                                                                                                                                                                                                                     RRFNEIQFWVVTEICLCSQLSKRVQLLKKFIKIAAHCKEYKNLNSFFAIVMGLSNIAVSR 715
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6
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                                                                                                                                                                                                                                                                                                                                                               4.6%;
Similarity 25.6%;
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Cloning and analysis of the full length human
ras-specific nucleotide exchange factor.
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Oncogene (1993) 8:1477-1485
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#formal_name Homo sapiens #common_name man
19-Jul-1996 #sequence_revision 19-Jul-1996 #text_change
10-Sep-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Schweighoffer, F.; Faure, M.; Fath, I.; Chevallier-Multon, M.C.; Apiou, F.; Dutrillaux, B.; Sturani, E.; Jacquet, M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Wei, W.; Mosteller, R.D.; Sanyal, P.; Gonzales,
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#domain CDC25-type guanine nucleotide exchange activator homology #label SOS
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Pred. No. 6.36e-26;
49; Mismatches 66; Indels
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                                                                                                                                                                                                                             #authors Bowtell, D.; Fu, P.; Simon, M.; Senior, P.
#journal Proc. Natl. Acad. Scl. U.S.A. (1992) 89:6511-6515
#title Identification of murine homologues of the Drosophila
#title sevenless gene: potential activators of ras.
#cross-references_MUID:92335328
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#journal Nature (1990) 344:355-357
#title Homologous activators of ras in fission
#cross-references MUID:90190870
#accession $28098
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                                                                                                             ##cross-references EMBL:Z11664; NID:g54136; PID:g54137
FICATION #superfamily CDC25-type guanine nucleotide
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##cross-references EMBL:X53254; N
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Local Similarity 22.2%;
nes 57; Conservation
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                                                                                                                                                                                                                                                                                                                                                                 $25714 #type fragment
son-of-sevenless-2 protein - mouse (fragment)
#formal_name Mus musculus #common_name house mouse
13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change
17-Mar-1999
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#formal_name Schizosaccharomyces pombe
17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change
09-Sep-1997
#length
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                 #domain pleckstrin repeat homology #label PLK\
#domain CDC25-type guanine nucleotide exchange homology #label SOS
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                                                                                             pleckstrin repeat homology
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#checksum 7302
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Pred. No. 1.89e-24;
75; Mismatches 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ##status preliminary; not compared with conceptual translation
##molecule_type mRNA
##residues 1-1333 ##label CHA
##rote sequence extracted from NCBI backbone (NCBIP:132148)
##note #superfamily CDC25-type guanine nucleotide exchange activated the homology; pleckstrin repeat homology
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                                                               LLIKDMTFTHEGN-KTFI--DN-LVNFEKMRMIANTARTVRYYRSQPF
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                                                                                  IYLTNILKTEEGNPEVLKRHGKELINFSKRRKVAEITGEIQQYQNQPY
                                                                                                                               IVMGLSNIAVSRLALTWEKLPSKFKKFYAEFESLMDPSRNHRAYRLTVAKLEPPLIPFMP
                                                                                                                                                  VVSAMNSSPVYRLDHTFEQIPSRQKKILEEAHELSE-DHYKK-YLAKLRSINPPCVPFFG
                                                                                                                                                                                            FKKTTANLDLFLRRFNEIQFWVVTEICLCSQLSKRVQLLKKFIKIAAHCKEYKNLNSFFA 703
                                                                                                                                                                                                                            KEINSPNLLKMIRHTTNLTLWFEKCIVETENLEERVAVVSRIIEILQVFQELNNFNGVLE 873
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                                                                                                                                                                                                                                                                                                                         h 4.1%;
Similarity 25.4%;
58; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chardin, P.; Camonis, J.H.; Gale, Schlessinger, J.; Wigler, M.H.; Science (1993) 260:1338-1343
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03-Mar-1994 #sequence_revision 18-Nov-1994
18-Mar-1997
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llarity 24.9%;
Conservative
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#domain CDC25-type guanine nucleotide exchange
homology #label SOS
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Pred. No. 1.67e-22;
70; Mismatches 92;
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##cross-references EMBL:M94160; NID:g170834; PID:g170835
FICATION #superfemily SH3 homology; CDC25-type guanine nucleotide
exchange activator homology
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#formal_name Candida albicans
20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change
09-Sep-1997
                                                                                                                                                                                                                                                                                                                                                  probable ras activator
#formal_name Mus musculus #common_name house mouse
13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change
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A Candida albicans homolog of CDC25
                                                                                                                                                                                                               Bowtell, D.; Fu, P.; Simon, M.; Senior, P. Proc. Natl. Acad. Sci. U.S.A. (1992) 89:6511-6515 Identification of murine homologues of the Drosophila sevenless gene: potential activators of ras.
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#length 1336
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guanine nucleotide exchange factor son-of-sevenless
- mouse
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#domain CDC25-type guanine nucleotide exchange activator
homology #label SOS
               #domain pleckstrin repeat homology #label PIK\
#domain CDC25-type guanine nucleotide exchange activator
homology #label SOS
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#molecular-weight 152762 #checksum
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Pred. No. 2.03e-20;
60; Mismatches 87;
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Best Local Similarity 25.48;
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                                                                                                  #authors Daniel, J.H.
Curr. Genet. (1986) 10:879-885
#title The CDC25 "Start" gene of Saccharomyces cerevisiae:
sequencing of the active C-terminal fragment and
homologies with rhodopsin and cytochrome p450.
#cross-references MUID:88194639
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#accession A23444
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                                                                                                                                                                                                                                                        ##molecule_type DNA
#residues 1-496,'Y',498-953,'LSVIMNLSR',964-1589 ##label
##cross-references EMBL:X03579; NID:g3483; PID:g3484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ##molecule_type DNA
#residues 1-1589 ##label PAU
##cross-references EMBL:U17247; NID:g577216; PID:g577222; MIPS:YLR310c
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                                     ##molecule_type DNA
##residues 877-1589 ##label DAN
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##residues 1-1589 ##label
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                  ##cross-references EMBL:X03579
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Boy-Marcotte, E.; Jacquet,
EMBO J. (1986) 5:375-380
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                                                                                                                                                                                                                                                                                                                                                                                         Characterization, cloning and sequence analysis of the CDC25 gene which controls the cyclic AMP level of Saccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cell (1987) 48:789-799
The S. cerevisiae CDC25 gene product regulates
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  #formal_name Saccharomyces cerevisiae
31-Mar-1988 #sequence_revision 31-Mar-1993
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                                                                                    $43051
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Pred. No. 9.72e-21;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 1336;
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Best Local Similarity 25.5%;
Matches 71; Conservative
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1301-1542
Query Match
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                                                                            825-1066
                                                                                                                                                                                                                                                                                                                #title Rasl and a putative guanine nucleotide exchange factor perform crucial steps in signaling by the sevenless performs kinase.

#cross-references_MUID:92034991
                                                                                                                                                                                   #gene
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                                                                                                                                                                                                                          ##residues 1-1596 ##label
##cross-references GB:M77501; 1
                                                                                                                                                                                                                                                          ##molecule_type mRNA
                                                                                                                                                ##cross-references FlyBase:FBgn0001965
FICATION #superfamily CDC25-type guanine nucleotide exchange activator
                                                                                                                                                                                                                                                                                 ##status
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NITKEIANANTLINFVSHTIVKQADVKTRSKLTQYFVTVAQHCKELNNFSSMTAIVSALY 1405
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      guanine nucleotide exchange activator son-of-sevenless
  fruit fly (Drosophila melanogaster)
#formal_name Drosophila melanogaster
28-May-1992 #sequence_revision 28-May-1992 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          #length 1589
                                                                                                                                                                                     FlyBase:Sos
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Cell (1991) 67:701-716
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                                     #length
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                                                                                                                              homology; pleckstrin repeat homology
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#domain CDC25-type guanine nucleotide exchange activator
homology #label SOS
                                   #domain pleckstrin repeat homology #label PLK\
#domain CDC25-type guanine nucleotide exchange activator
homology #label SOS
|th 1596  #molecular-weight 177933  #checksum 4040
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SGD:S0004301; MIPS:YLR310c
   4.0%;
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   Score 251;
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NID:g158470;
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   DB
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   Length 1596
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RESULT
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Matches 48; Conservative
                                                                                                                                                                                                                 #authors
#journal
#title
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                                                                                                             #cross-references MUID:96405918
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NCE S69380
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NCE S64761
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##cross-references EMBL:Z73121; NII
MIPS:YLL016w
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              ##cross-references EMBL:X91488; NID:g1495203; PID:e199006;
                                     ##residues
                                                                            ##status
  ##note
                                                   ##molecule_type DNA
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                                                                                                                                                                                                                                                                                                                                                                    submitted to the EMBL Data Library, April 1996
The sequence of 32 kb on the left arm of yeast chromosome Xi
reveals 14 open reading frames among which HSP104, SSA2,
SPA2, KNS1, DPS1/APS, SDC25, a new member of the
seripauperins family and a new ABC transporter homologous
to the human multidrug resistance protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SCD25 protein (version 2) - yeast (Saccharo protein L1309; protein YLLO16w #formal_name Saccharomyces cerevisiae 01-aug-1995 #sequence_revision 24-May-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          S64758
SCD25 I
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$64743
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                                                                                                                                                     Sequence analysis of the CEN12 region of Saccharomyces cerevisiae on a 43.7 kb fragment of chromosome XII including an open reading frame homologous to the human cystic fibrosis transmembrane conductance regulator protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        S64764
                                                                                                                                                                                                                                    Miosga, T.; Zimmermann, F.K.
Yeast (1996) 12:693-708
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                                       1-1048 ##label MIW
the nucleotide sequence was
                                                                          nucleic acid sequence not shown;
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59;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NID: g1360186;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence Database,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              yeast (Saccharomyces cerevisiae)
    submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Database,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PID:e245452; PID:g1360187;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PID:e245452; PID:g1360187
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                      PID:g1495207
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Gaps

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Length 1250; Indels

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ALTERNATE_NAMES ORGANISM
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CLASSIFICATION
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REFERENCE
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#title
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#title
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 744-995
#map_position 12L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        #cross-references MUID:91094833
#accession S12942
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            #accession
                                                                                                                                                                                               #cross-references MUID:89306677
                                                                                                                                                                                                                                                                                                                                                                           #authors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  #authors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       676 SKRVQLLKKFIKIAAHCKEYKNLNSFFAIVMGLSNIAVSRLALTWEKLPSKFKKFYAEFE 735
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             736 SLMDPSRNHRAYRLTVAKLEP-PLIPFMPLLIKDMTFTHEGNKTFI 780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             876 KLMDPKKNFINYRNELKSLHSAPCVPFFGVYLSDLTFTDSGNPDYL 921
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            816 SKRAKLLSHFIFIAEYCRKFNNFSSMTAIISALYSSPIYRLEKTWQAVIPQTRDLLQSLN 875
                                                                                                                                                                                                                                                                                                                                                                                                                                              ##residues 1-737,'A',738-970,'I',972-1250 ##label DAM2
##cross-references EMBL:M26647
#horte the authors translated the codon GAG for residue 538 as
##note Asp, GTC for residue 550 as Asp, and CTA for residue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ##molecule_type DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ##cross-references SGD:S0003939; MIPS:YLL016w
                          ##cross-references SGD:S0003939; MIPS:YLL016w
                                                                                                                                                  ##residues
                                                                                                                                                                 ##molecule_type DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ##molecule_type DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ##cross-references EMBL:M26647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14
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Similarity 34.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Jacquet, M.
Mol. Cell. Biol. (1991) 11:202-212
SDC25, a CDC25-like gene, which contains a RAS-activating domain and is a dispensable gene of Saccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      S14177 #type complete
SCD25 protein (version 1) - yeast (Saccharomyces cerevi.
protein tl309; protein VLL016w
#formal_name Saccharomyces cerevisiae
02-Jun-1994 #sequence_revision 02-Jun-1994 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   #superfamily CDC25-type guanine nucleotide exchange activator
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         #domain CDC25-type guanine nucleotide exchange activator homology #label SOS #length 1048 #molecular-weight 121960 #checksum 2510
                                                                                                                                                                                                                                                                      The C-terminal part of a gene partially homologous to CDC25 gene suppresses the cdc25-5 mutation in Saccharomyces
                                                                                                                                                                                                                                                                                                                                              PS0041
Boy-Marcotte, E.; Damak, F.; Camonis, J.; Garreau, Jacquet, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            submitted to the EMBL Data Library, August 1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      S14177; S12942; PS0040
S14177
                                               SGD:SCD25; SDC25
                                                                                                                                                                                                                                                                                                                           Gene (1989) 77:21-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Damak, F.; Boy-Marcotte, E.; Le-Roscouet, D.; Guilbaud,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Damak, F.; Boy-Marcotte, E.; Le-Roscouet, D.; Guilbaud,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SGD:SCD25; SDC25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                    cerevisiae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         06-Feb-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Jacquet,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              homology
                                                                                               668-679, 'NPVMTILMC', 689,'N', 691-1250 the authors translated the codon GCA Asp and GAT for residue 748 as Ala
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         l-1250 ##label DAM1
                                                                                                                                                                                                                                                                                                                                                                                                                      Asp, GTC I
804 as Lys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Library, September 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 240; DB 2;
Pred. No. 2.32e-18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches 43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   yeast (Saccharomyces cerevisiae)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 1048;
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                                                                                                                          ##label BOY
for residue 747
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TITLE
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946-1197
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                             SUMMARY
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                                                                                                                                                                                                                                                                                                                                                 FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                        KEYWORDS
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Best Local
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                                               199,208
323,332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      #journal
#title
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              #authors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         #cross-references_MUID:92153429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1078 KLMDPKKNFINYRNELKSLHSAPCVPFFGVYLSDLTFTDSGNPDYL 1123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1018 SKRAKLLSHFIFIAEYCRKFNNFSSMTDIISALYSSPIYRLEKTWQAVIPQTRDLLQSLN 1077
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ##cross-references EMBL:X62382; NID:g5587; PID:g5588

#mote this protein is identified as the N4 isoform

The inactive form of the enzyme is composed of two regulatory

chains and two catalytic chains. Activation by cAMP produces two

active catalytic monomers and a regulatory dimer that binds four
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     736 SLMDPSRNHRAYRLTVAKLEP-PLIPFMPLLIKDMTFTHEGNKTFI 780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       676 SKRVQLLKKFIKIAAHCKEYKNLNSFFAIVMGLSNIAVSRLALTWEKLPSKFKKFYAEFE 735
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ##residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ##molecule_type mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The pseudophosphorylation site binds to the substrate-binding region of the catalytic chain but is not phosphorylated. The physiological significance of phosphorylations by other kinases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Type I regulatory chains contain a high-affinity binding site for \mathsf{MgATP} .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 h 3.8%;
Similarity 33.0%;
35; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CAMP molecules.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           unclear.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bergold, P.J.; Beushausen, S.A.; Sacktor, T.C.; Cheley, S.;
Bayley, H.; Schwartz, J.H.
Neuron (1992) 8:387-397
A regulatory subunit of the cAMP-dependent protein kinase
down-regulated in aplysia sensory neurons during long-term
sensitization.
                     form) #status predicted\
#binding_site cAMP (Glu, Arg) #status predicted\
#binding_site cAMP (Glu, Arg) #status predicted
#binding_site cAMP (Glu, Arg) #status predicted
#length 378 #molecular-weight 42737 #checksum 2977
                                                                                                                                                                                                                                                                                                                                                                                           acetylated amino end; ATP binding; cAMP binding; duplication;
heterotetramer; homodimer; phosphoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         JH0590
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OKGARI #type complete
protein kinase (EC 2.7.1.37), cAMP-dependent, type I
regulatory chain - California sea hare
#formal_name Aplysia californica #common_name California sea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           *superfamily CDC25-type guanine nucleotide exchange activator
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   #superfamily cAMP-dependent protein kinase regulatory chain; cAMP receptor protein cyclic nucleotide-binding domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   #length 1250 #molecular-weight 144779 #checksum
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                                                                                                                                                                                            #product protein kinase, cAMP-dependent, type I-beta
regulatory chain *status predicted *label MAT\
#domain protein interaction #label DIM\
#region pseudophosphorylation motif\
#domain cAMP receptor protein cyclic nucleotide-binding
domain homology *label CAI\
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1-378 ##label BER
                                                                                                                    #domain cAMP receptor protein cyclic nucleotide-binding
domain homology #label CA2\
#modified_site acetylated amino end (Ala) (in mature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 236; DB 2;
Pred. No. 9.82e-18;
26; Mismatches 44
```

GENETICS

#gene

RESULT

TITLE

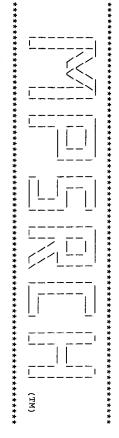
DATE

γ 멍 δÃ Ъ SUMMARY

FEATURE

GENETICS

1



Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Sat Apr 22 13:23:13 2000; MasPar time 14.86 Seconds 759.883 Million cell updates/sec

Tabular output not generated.

Title: >US-09-422-999-18 (1-849) from US09422999.pep

Sequence: Description: Perfect Scor Score: 1 MVLWKRALTMTGFLTRRTHL.....VIDNQRTLSQMSHRLEPRRP 849

Scoring table: PAM 150 Gap 11

134018 seqs, 13297625 residues

Searched:

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

Statistics: Mean 36.052; Variance 179.682; scale 0.201

1:5A_COMB 2:5B_COMB 3:6_COMB 4:PCT9_COMB 5:backfiles1

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. derived by analysis of the total score distribution.

SUMMARIES

5 7 7 11 11 11 11 11 11 11 11 11 11 11 11	4321	Result
276 266 266 256 256 255 255 255 251 251 143 1143 1143 1133 1133 1133 1133	287 287 287 287 276	Score
222222334444444444	4444	% Query Match I
652 423 364 423 423 426 1319 1336 1336 436 1336 436 1336 768 852 768 852 768 852 768	489 666 814 402	Length [
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8, 11, 5, 5, 12, 13, 14, 10,	Sequence 4, 1 Sequence 3, 1 Sequence 2, 1 Sequence 14,	Description
Applicatio	Applicatio Applicatio Applicatio Applicatio	
5.279e-12 5.22e-11 5.22e-11 3.07e-10 3.67e-10 3.67e-10 3.67e-10 7.43e-10 7.43e-10 7.43e-10 7.43e-02 6.37e-02 6.37e-02 6.37e-02 6.37e-02 6.37e-01 1.67e+00 1.67e+00 1.67e+00 1.67e+00	1.23e-12 1.23e-12 1.23e-12 1.23e-12 8.79e-12	Pred. No.

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5.68e+01	5.68e+01	5.68e+01	5.68e+01	3.21e+01	3.21e+01	3.21e+01	3.21e+01	6.53e+01	3.71e+01	4.93e+01	6.53e+01	6.53e+01	5.68e+01	5.68e+01	1.81e+01	2.63e+00	4.13e+00	2.26e+00	1.67e+00	1.6/e+00

ALIGNMENTS

RESULT Sequence 4, Application US/08318831 XXXXXX US-08-318-831-4 Sequence 4, Application US/08318831 Patent No. APPLICANT: Schweighofter,
APPLICANT: Tocque, Bruno
TITLE OF INVENTION: PEPTIL
TITLE OF INVENTION: PREPTIL
TITLE OF INVENTION: PREPTIL
TITLE OF INVENTION: PREPTIL
TITLE OF INVENTION: PREPTIL GENERAL NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS: ADDRESSEE: INFORMATION: E: Rhone-Poulenc 500 Arcola Road, Schweighoffer, Fabien STANDARD; PEPTIDES HAVING A GDP EXCHANGE FACTOR ACTIVITY, NUCLEIC ACID SEQUENCES CODIPERPARATION AND UTILIZATION Rorer Inc. 3C43 PRT; 489 AA ACID SEQUENCES CODING FOR SAID PEPTID

TELEFAX: (610) 454-38 INFORMATION FOR SEQ ID NO: APPLICATION NUMBER: FR92/04827
FILING DATE: 21-APR-1992
ATTORNEY/AGENT INFORMATION:
NAME: Smith, Julie K.
REGISTRATION NUMBER: p-38,619
REFERENCE/DOCKET NUMBER: ST9203:
TELECOMMUNICATION INFORMATION: COMPUTER: Macintosh
OPERATING SYSTEM: System 7.1
SOFTWARE: Word 5.1 (EPO Patentin)
CURRENT APPLICATION DATA: ZIP: 19426 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy SEQUENCE CHARACTERISTICS: PRIOR APPLICATION DATA: STREET: 500 Arcola I
CITY: Collegeville
STATE: PA
COUNTRY: USA APPLICATION NUMBER: FILING DATE: 19 Oct TELEPHONE: CLASSIFICATION: 1: (610) 454-3839 (610) 454-3808 OR SEQ ID NO: 4: Floppy disk JMBER: US/08/318,831 19 October 1994 ST92033-US

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Query Match
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Best Local Similarity 25.6%;
Matches 40; Conservative
                        SEQUENCE
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                                                                  TELEFAX: (610) 454-3808 INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Macintosh
OPERATING SYSTEM: System
SOFTWARE: Word 5.1 (EPO
                                                                                                             REFERENCE/DOCKET NUMBER: ST
                                                                                                                                                APPLICATION NUMBER: FR92, FILING DATE: 21-APR-1992 ATTORNEY/AGENT INFORMATION: NAME: Smith Julie K.
                                                                                                                                                                                             CLASSIFICATION: 435 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Tocque, Bruno
TITLE OF INVENTION: PEPT:
TITLE OF INVENTION: ACTITITLE OF INVENTION: PREP
                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
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                                              TYPE:
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                                                                                                    TELEPHONE:
                                                                                                                                                                                                                                                                                                                                           STREET: 500 Arcola CITY: Collegeville
                                                                                                                                       REGISTRATION NUMBER:
                                                                                                                                                                                                                     APPLICATION NUMBER: FILING DATE: 19 Oct
                       TOPOLOGY: 1:
CE 666 AA;
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                                                       LENGTH:
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489 AA; 55488 MW;
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                       75236 MW; 2256870 CN;
                                                                                                                                                                                                                     19 October 1994
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ACTIVITY, NUCLEIC ACID SEQUENCES CODING FOR SAID PEPTIDES
PREPARATION AND UTILIZATION
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Score 287; DB 1;
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Pred. No. 1.23e-12;
49; Mismatches 66
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                                                                                                                                               TELEFAX: (610) 454-3808 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                     SEQUENCE CHARACTERISTICS
                                                                                                                                                                     REFERENCE/DOCKET NUMBER: ST
TELECOMMUNICATION INFORMATION:
TELEPHONE: (610) 454-3839
                                                                                                                                                                                                                   FILING DATE: 21-APR-1992
ATTORNEY/AGENT INFORMATION:
NAME: Smith, Julie K.
                                                                                                                                                                                                                                                       CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                  SOFTWARE: Word 5.1 (EPO Patentin) CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Schweighoffer, APPLICANT: Tocque, Bruno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
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                                                                                                                                                                                                         NAME: Smith, Julie I REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: FILING DATE: 19 Oct
                                                                                                                                                                                                                                                                                                                                                        COMPUTER:
                                                                                   TOPOLOGY: linear
CE 814 AA; 91292 MW; 3388819 CN;
                                                                                                                      LENGTH:
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                                                  Similarity
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0 Arcola Road, 3C43
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ACTIVITY, NUCLEIC ACID SEQUENCES CODING FOR SAID PEPTID
PREPARATION AND UTILIZATION
                                                                                                                                                                                                                                                                                                                                         System 7.1
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                                    Score 287; DB 1;
Pred. No. 1.23e-12;
49; Mismatches 66
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                                                                                                                                SEQUENCE
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584 EQFDSLTPLPEQEGPTVGTVGTVFELMSSKDLAYQMTIYDWELFNCVHELELIYHTFGRHN 643
                            146 QELEDLS-LHNSPDPIIYKDELVLLLPPREIAKQLCILEFQSFSHISRIQFLTKIWDELN 204
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                                                              Local Similarity
nes 57; Conser
                                                                                                                                                                                                          TELEFAX: (202) 293-7860
TELEX: 6491103
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: ITTLE OF INVENTION: ITTLE OF INVENTION: INUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: PL0921/92
FILING DATE: 17-FEB-1992
                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/AU93/00068
FILING DATE: 17-FEB-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC COMPAI
OPERATING SYSTEM: PC-DO
SOFTWARE: PATENTIN Rela
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
                                                                                                                                            MOLECULE TYPE:
                                                                                                                                                                                                                                                                         REGISTRATION NUMBER: 30,764
REFERENCE/DOCKET NUMBER: Q-36066
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 293-7060
                                                                                                                                                                                                                                                                                                                                              FILING DATE: 17-FEB-1992
ATTORNEY/AGENT INFORMATION:
NAME: KIT, GORDON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
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                                                                                                                                                          TYPE: ami
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/290,731C FILING DATE: 17-OCT-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & STREET: 2100 PENNSYLVANIA AVENUE, N.W.
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402 AA; 47252 MW; 844812 CN;
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llarity 22.2%;
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SYSTEM: PC-DOS/MS-DOS
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DNA MOLECULES ENCODING MURINE
SON OF SEVENLESS (mSOS) GENE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Release #1.0, Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15
                                                            Score 276; DB 2; Le
Pred. No. 8.79e-12;
75; Mismatches 119;
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                                                                                          Length 402
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                                                            Gaps
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                                                                            RESULT
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          Query Match 4.4%;
Best Local Similarity 25.8%;
Matches 59; Conservative
                                                                            SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                       TELEFAX: (610) 454-3808
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 652 amino acids
                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR92/04827
FILING DATE: 21-APR-1992
ATTORNEY/AGENT INFORMATION:
NAME: Smith, Julie K.
REGISTRATION NUMBER: P-38,619
                                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM: System 7.1
SOFTWARE: WORD 5.1 (EPO Patentin)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/318,831
FILING DATE: 19 October 1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Macintosh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: TOCQUE, Bruno
TITLE OF INVENTION: PETITIES HAVING A GDP EXCHANGE FACTOR
TITLE OF INVENTION: ACTIVITY, NUCLEIC ACID SEQUENCES CODING FOR SAID PEPTID
TITLE OF INVENTION: PREPARATION AND UTILIZATION
NUMBER OF SEQUENCES: 12
                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: ST
TELECOMMUNICATION INFORMATION:
TELEPHONE: (610) 454-3839
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
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                                                                                            TYPE: ami TOPOLOGY:
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                                                                            652 AA; 74235 MW; 2320730 CN;
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                                                                                                          amino acid
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00 Arcola Road, 3C43
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          Score 276; DB 1; 1
Pred. No. 8.79e-12;
71; Mismatches 89
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                                          Length 652;
            Indels 10;
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Query Match
                                                                          REGISTRATION NUMBER: 30,764
REFERENCE/DOCKET NUMBER: Q-36066
TELECOMUNICATION INFORMATION:
TELEPHONE: (202) 293-7060
TELEPAX: (202) 293-7860
TELETAX: (202) 293-7860
TELEX: 6491103
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
                       SEQUENCE
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APPLICANT: BOWTEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                  MOLECULE TYPE:
                                                                                                                                                                                FILING DATE: 17-FEB-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                        PRIOR APPLICATION DATA: PCT/AU93/00068
                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GIYLTNILKTEEGNNDFLKKKGKDLINFSKRRKVAEITGEIQQYQNQPY 334
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IVMGLSNIAVSRLALTWEKLPSKFKKFYAEFESLMDPSRNH-RAYRLTVAKLEPPLIPFM 762
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                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC
OPERATING SYSTEM:
SOFTWARE: Patentl
                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/0 FILING DATE: 17-OCT-1994
                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 2100 PEN CITY: WASHINGTON
                                                                                                                                                                                            APPLICATION NUMBER: PL09 FILING DATE: 17-FEB-1992
                                                                                                                                                                                                                                FILING DATE:
                                                                                                                                                                                                                                                                 CLASSIFICATION:
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                                                                LENGTH:
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                                                     amino acid
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                    YPE: protein
AA; 49877 MW; 918596 CN;
                                                                  423 amino acids
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                                                                                                                                                                                                                                                                                                         IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                             Floppy disk
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4.38;
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Score 266;
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DB
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Length 423;
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Matches 57; Conservative
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                                                              TELEFAX: (202) 293-78
TELEX: 6491103
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: BOWTEL
                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/290,731
FILING DATE: 17-OCT-1994
                                                                                                                                                                                                           APPLICATION NUMBER: PCT/AU93/00068 FILING DATE: 17-FEB-1993 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                       ZIP: 20037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                    SEQUENCE CHARACTERISTICS:
LENGTH: 1297 amino aci
                                                                                                                                                         APPLICATION NUMBER: PL0921/92
FILING DATE: 17-FEB-1992
ATTORNEY/AGENT INFORMATION:
NAME: KIT, GORDON
                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                  REFERENCE/DOCKET NUMBER: Q-
TELECOMMUNICATION INFORMATION:
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               TOPOLOGY:
                          TYPE: amino acid
                                                                                                     TELEPHONE:
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                                                                                                                                             REGISTRATION NUMBER:
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                                       1297 amino acids
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                                                                                         (202) 293-70
                                                                                                                                                                                                                                                                                                                                                                                               USA
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                                                                                                                                                                                                                                                                                                                                                          Floppy disk
protein
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                                                                                                        293-7060
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                                                                                                                                             30,764
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                                                                 4.
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             586
                                 TELEPHONE: (610) 454-3839
TELEFAX: (610) 454-3808
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Match 4.3%;
Local Similarity 24.9%;
                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                      REGISTRATION NUMBER: P-38,6
REFERENCE/DOCKET NUMBER: ST
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                       APPLICANT: Tocque, Bruno TITLE OF INVENTION: PEPTI TITLE OF INVENTION: ACTIV TITLE OF INVENTION: PREPA
                                                                                              FILING DATE: 21-APR-1992
ATTORNEY/AGENT INFORMATION:
NAME: Smith, Julie K.
                                                                                                                                    CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                        COMPUTER: Macintosh
OPERATING SYSTEM: System 7.1
SOFTWARE: Word 5.1 (EPO Pate)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                   APPLICANT:
                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GIYLTNILKTEEGNSDFLKRKGKDLINFSKRRKVAEITGEIQQYQNQPY 942
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FKKTTANLDLFLRRFNEIQFWVVTEICLCSQLSKRVQLLKKFIKIAAHCKEYKNLNSFFA 703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FDSLTPLPEQEGPTVGTVGTFELMS--SKDLAYQMTIYDWELFNCVHELELIYHTFGRHN 643
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PLLIKDMTFTHEGNKTFI----D-NLVNFEKMRMIANTARTVRYYRSQPF 807
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                                                                                                                                                                                                                                        STATE:
COUNTRY:
                TYPE: amino acid
                                                                                                                  APPLICATION NUMBER: FR92 FILING DATE: 21-APR-1992
                                                                                                                                                       APPLICATION NUMBER: FILING DATE: 19 Oct
         TOPOLOGY:
                                                                                                                                                                                                                                                                             ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  57;
                                                                                                                                                                                                                                                                                                                                                                     6, Application
364 AA; 41968 MW; 717826 CN;
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                                                                                                                                                                                                                                 19426
                                                                                                                                                                                                                                                           Collegeville
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500 Arcola Road,
                          364 amino acids
                                                                                                                                                                                                                                         USA
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                                                                                                                                                        19 October 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                      PEPTIDES HAVING A GDP EXCHANGE FACTOR ACTIVITY, NUCLEIC ACID SEQUENCES CODING FOR SAID PEPTIDES PREPARATION AND UTILIZATION
                                                                                                                                                                                                                                                                                                                                                                      US/08318831
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                                                                                                                             FR92/04827
                                                                                                                                                                                  (EPO Patentin)
                                                                                                                                                                US/08/318,831
                                                                                P-38,619
ER: ST92033-US
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Pred. No. 5.22e-
70; Mismatches
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3C43
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Query Match
Best Local Similarity
Matches 58; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           764 LLIKDMTFTHEGN-KTFI--DN-LVNFEKMRMIANTARTVRYYRSQPF 807
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                                                   TELEFAX: (202) 293-78
TELEX: 6491103
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION:
TITLE OF INVENTION:
                               SEQUENCE CHARACTERISTICS:
                                                                                                                    REFERENCE/DOCKET NUMBER: Q-
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                      APPLICATION NUMBER: PL09
FILING DATE: 17-FEB-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                             FILING DATE: 17-FEB-PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FQSSPPTVEWHISRPGHIETFDLLTLHPIBIARQLTLLDSDLYRAVQPSDLVGSVWTKED 81
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                                                                                                                                                                                                                                                                                                                  FILING DATE: 17 CLASSIFICATION:
                                                                                                    TELEPHONE:
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                                                                                                                                                           REGISTRATION NUMBER:
                                                                                                                                                                           NAME:
                                                                                                                                                                                                                                                                                APPLICATION NUMBER: PCT/AU93/00068
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE:
                LENGTH:
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: 423 amino acids amino acid
                                                                                                                                                                           KIT, Gordon
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUGHRUE,
                                                                                     (202) 293-70
202) 293-7860
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25.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Floppy disk
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                                                                                                                                                                                                                                                                                                                                      17-OCT-1994
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                                                                                                         293-7060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     David Douglas Lawrence
DNA MOLECULES ENCODING N
SON OF SEVENLESS (mSOS)
AND mSOS POLYPEPTIDES
                                                                                                                                                                                                                            PL0921/92
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                                                                                                                                                       30,764
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Pred. No. 3.07e-10;
65; Mismatches 97;
                                                                                                                                          36066
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                                                                                                                                                                                                                                                                                                                                                                                          Version
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 12, Application US/08290731C
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 12, Apprin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       332 IYLTNILKTEEGNPEVLRRHGKELINFSKRRRVAEITGEIQQYQNQPY 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 154 FQSSPPTVEWHISRPGHIETFDLLTLHPIEIARQLTLLESDLYRAVQPSELVGSVWTKED 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      764 LLIKDMTFTHEGN-KTFI--DN-LVNFEKMRMIANTARTVRYYRSQPF 807
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   644 FKKTTANLDLFLRRFNEIQFWVVTEICLCSQLSKRVQLLKKFIKIAAHCKEYKNLNSFFA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 586 FDSLTPLPEQEGPTVGTVGTFELMS--SKDLAYQMTIYDMELFNCVHELELIYHTFGRHN 643
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Local Similarity 25.48;
nes 58; Conservation
                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: BOWTELL, David Douglas Lawrence TITLE OF INVENTION: DNA MOLECULES ENCODING | TITLE OF INVENTION: SON OF SEVENLESS (mSOS) TITLE OF INVENTION: AND mSOS POLYPEPTIDES
                                                                                                                                                                                                                      SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA:
                                                TELECOMMUNICATION INFORMATION:
                                                                                                ATTORNEY/AGENT INFORMATION:
                                                                                                                                  PRIOR APPLICATION DATA:
                                                                                                                                                                        PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KEINSPNLLKMIRHTINLTLWFEKCIVETENLEERVAVVSRIIEILQVFQELNNFNGVLE 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IVMGLSNIAVSRLALTWEKLPSKFKKFYAEFESLMDPSRNHRAYRLTVAKLEPPLIPFMP 763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VVSAMNSSPVYRLDHTFEQIPSRQKKILEEAHELSE-DHYKK-YLAKLRSINPPCVPFFG 331
                                                                                                                                                                                                                                                                                                                       STREET: 210,
CTTY: WASHINGTON
                                                                                                                                             APPLICATION NUMBER: PCT/A
                                                                                                                                                                                                                                            COMPUTER: IBM PC
OPERATING SYSTEM:
                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                      REGISTRATION NUMBER: 30,764
                                                                                                                                                                                                APPLICATION NUMBER: US/08/290,731C FILING DATE: 17-OCT-1994
                         TELEFAX:
                                   TELEPHONE:
                                                              REFERENCE/DOCKET NUMBER:
                                                                                      NAME:
                                                                                                            APPLICATION NUMBER: PL0921/92 FILING DATE: 17-FEB-1992
                                                                                                                                                                                      CLASSIFICATION:
                                                                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE:
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                                                                                    KIT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Application US/08290731C
               6491103
                         E: (202) 293-70
(202) 293-7860
                                                                                                                                                                                                                                                                                                           USA
                                                                                                                                                                                                                                                                                                                                              3: SUGHRUE, MION, ZINN, MACPEAK & SEAS 2100 PENNSYLVANIA AVENUE, N.W.
                                                                                    Gordon
  SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                      293-7060
                                                                                                                                                            PCT/AU93/00068
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Pred. No. 3.67e-10;
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                                                              Q-36066
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      XXXXXX
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2,
                                                                                                                                                                                                                                                                                                                                                                             Patent No. GENERAL II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    710
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                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2, Application Patent No. 5843646
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                                            OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Vers
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/290,731C
FILING DATE: 17-CCT-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION UMBER: PCT/AU93/00068
FILING DATE: 17-FEB-1993
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               769 MTFTHEGNKTFI-D--NLVNFEKMRMIANTARTVRYYR 803
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       537 VADKLGSGEGLI--IV-KMSSGGEKVVLKPNDV-SVFTTLTINGRLFACPREQFDSLTPL 592
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                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION:
TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 426 amino acid
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
            ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NIAVSRLALTWEKLPSKFKKFYAEFESLMDPSRNHRAYR-LTVAKLEPPLIPFMPLLIKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SSPIYRLKKTWDLVSTESKDLLKNLNNLMDSKRNFVKYRELLRSVTDVACVPFFGVYLSD 345
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                                                                                                                                                                                                                      STATE: I
COUNTRY:
ZIP: 200
                        FILING DATE:
                         APPLICATION NUMBER: PLOS
FILING DATE: 17-FEB-1992
                                                                                                                                                                                                                                                          STREET: 2100 PEN
CITY: WASHINGTON
                                                                                                                                                                                                                                                                                    ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4.1%;
Similarity 25.5%;
71; Conservati
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426 AA; 49080 MW; 1001703 CN;
                                                                                                                                                                                                                                                                                                                                                                             INFORMATION:
                                                                                                                                                                                                                       20037
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                                                                                                                                                                                                                                  USA
                                                                                                                                                                                                                                                                                                                                                                 BOWTELL,
                                                                                                                                                      PatentIn Release #1.0, Version #1.
Gordon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                          David Douglas Lawrence
DNA MOLECULES ENCODING
SON OF SEVENLESS (mSOS)
AND mSOS POLYPEPTIDES
                                                                                                                                                                                                                                                                                                                                                                                                       US/08290731C
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                                    PL0921/92
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Pred. No. 3.67e-10,
77; Mismatches 11
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REFERENCE/DOCKET NUMBER:

REGISTRATION NUMBER:

30,764

Q-36066

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Best Local (
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MOLECULE TYPE: protein
SEQUENCE 1319 AA; 150882 MW;
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TELEPHONE: (202) 293-7060
TELEFAX: (202) 293-7860
TELEX: 6491103
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: BOWTELL, DAV
TITLE OF INVENTION: DNA
TITLE OF INVENTION: SON
TITLE OF INVENTION: AND
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
                                                                                        APPLICATION NUMBER: US/0:
FILING DATE: 17-OCT-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAtentin Release #1.0, Version
CURRENT APPLICATION DATA:
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LENGTH: 1319 amino aci
     PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                            STREET: ZIV
                                                APPLICATION NUMBER: PCT//
FILING DATE: 17-FEB-1993
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Similarity 25.48;
58; Conservation
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DNA MOLECULES ENCODING MURINE
SON OF SEVENLESS (mSOS) GENE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US/08290731C
                                                                            PCT/AU93/00068
                                                                                                                                                                       us/08/290,731C
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     PL0921/92
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Pred. No. 3.
64; Mismatc
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.67e-10;
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Query Match
Best Local Similarity
Watches 58; Conserv
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                                                                                                                                                                                                                                                                            Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                             TITLE OF INVENTION: DNA
TITLE OF INVENTION: SON
TITLE OF INVENTION: AND
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION: TELEPHONE: (202) 293-7060 TELEFAX: (202) 293-7860
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/0
FILING DATE: 17-OCT-1994
                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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ATTORNEY/AGENT INFORMATION:
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                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
                                                                                                                                     COUNTRY:
                                                                                                                                                             STREET: 2100 PEN
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                                                                                                                             ZIP:
                                                                                                                                                   STATE:
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                                                                                                                                                                                    ADDRESSEE:
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5. 5843646
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1336 AA; 152734 MW; 9610574 CN;
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                                                                                                                                                 D.C.
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                                                                                                                                        USA
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25.4%;
                                                                                                     Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                     SON
AND
                                                                                                                                                                                                                                            David Douglas
  PCT/AU93/00068
                                               us/08/290,731C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 255; DB 2;
Pred. No. 3.67e-10;
64; Mismatches 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30,764
                                                                                                                                                                                                                                MOLECULES ENCODING MURINI OF SEVENLESS (mSOS) GENE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6:
                                                                                                                                                                                                                      MSOS POLYPEPTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q-36066
                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                     Lawrence
                                                                                                                                                                                                                                                                                                                                                                                    430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       98;
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                                                                     #1.25
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Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                 Sequence 5, Application US/08290731C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         613 DLAYOMTIYDWELFNCVHELELIYHTFGRHNFKKTTANLDLFLRRFNEIQFWVVTEICLC 672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    192 ELARQLTLLEFEMYKNVKPSELVGSPWTKKDKEVKSPNLLKIMKHTTNVTRWIEKSITEA 251
                                                                                                                                                                                                                                                                                                     Patent No. 5843646
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                791 MIANTARTVRYYRSQPF 807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            370 KVAEIIGEIQQYQNQPY 386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (202) 293-7860
TELEX: 6491103
INFORMATION FOR SEQ ID NO: 9:
                                                                                                                                                                                                                              APPLICANT: BOWTELL,
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA:
                                                            COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS
LENGTH: 430 amino acid
                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ENYEERLAIMQRAIEVMMVMLELNNFNGILSIVAAMGTASVYRLRWTFQGLPERYRKFLE 311
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ECRELSD-DHLKK-YQERLRSINPPCVPFFGRYLTNILHLEEGNPDLLANTELINFSKRR 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SQLSKRVQLLKKFIKIAAHCKEYKNLNSFFAIVMGLSNIAVSRLALTWEKLPSKFKKFYA
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                                                                                                                                                                   STREET: 2100 PENICITY: WASHINGTON
                     APPLICATION NUMBER:
                                                                                                                                       COUNTRY:
                                                                                                                                                                                                ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: PL0921/92 FILING DATE: 17-FEB-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REGISTRATION NUMBER: 30 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE:
                                                                                                                                                                                                                                                                                                                       5, Application US/08290731C
o. 5843646
                                                                                                                20037
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430 AA; 50634 MW; 939381 CN;
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                                                                                                                                                        D.C
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                                                                                                                                                                                                                                             BOWTELL, David Douglas Lawrence
JENTION: DNA MOLECULES ENCODING I
SON OF SEVERLESS (MSOS)
JENTION: AND MSOS POLYPEPTIDES
                                                                                                                                                                                                   SUGHRUE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gordon
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24.4%;
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       17-OCT-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                  us/08/290,731C
                                                                                                                                                                                                   MION,
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Pred. No. 7.43e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q-36066
                                                                                                                                                                                   ZINN, MACPEAK & SEAS AVENUE, N.W.
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Best Local
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                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: BOWTELL, I
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                         US-08-290-731C-13
                                                                                                                                                                                                                                                                                                                   Sequence 13, Application US/08290731C
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                                                                                                                                                                                                                                                                       Sequence 13, Application Patent No. 5843646
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  791 MIANTARTVRYYRSQPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (202) 293-780
TELEX: 6491103
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                     ZIP: 20037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: Q-
TELECOMMUNICATION INFORMATION
TELEPHONE: (202) 293-7060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION: NAME: KIT, Gordon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: PL092
FILING DATE: 17-FEB-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/AU93/00068
FILING DATE: 17-FEB-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SQLSKRVQLLKKFIKIAAHCKEYKNLNSFFAIVMGLSNIAVSRLALTWEKLPSKFKKFYA 732
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ENYEERLAIMQRAIEVMMVMLELNNFNGILSIVAAMGTASVYRLRWTFQGLPERYRKFLE 951
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ECRELSD-DHLKK-YQERLRSINPPCVPFFGRYLTNILHLEEGNPDLLANTELINFSKRR 1009
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amir
 OPERATING SOFTWARE:
                                                                                                                   ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & STREET: 2100 PENNSYLVANIA AVENUE, N.W. CITY: WASHINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH:
                              COMPUTER:
                                                                                         STATE: D.C. COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REGISTRATION NUMBER: 30,764
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        48;
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1572 AA; 174116 MW;
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IBM PC compatible SYSTEM: PC-DOS/MS-DOS PatentIn Release #1.0,
                                                                                           USA
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                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  807
                                                                                                                                                                                            David Douglas Lawrence
DNA MOLECULES ENCODING N
SON OF SEVENLESS (mSOS)
AND mSOS POLYPEPTIDES
                                                                                                                                                                                                                                                                                     US/08290731C
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59; M
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Pred. No. 7.43e-10
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 Version #1.
                                                                                                                                                                                                                                                                                                                                                                                                         418
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CC CURRENT APPLICATION DATA:

CC APPLICATION UNMBER: US/08/290,731C

CC FILING DATE: 17-057-1994

CC PRIOR APPLICATION: 435

CC PRIOR APPLICATION UNMBER: PCT/AU93/00068

CC PRIOR APPLICATION UNMBER: PL0921/92

CC ATTONNEY AGAIN INFORMATION:

CC APPLICATION NUMBER: D10921/92

CC ATTONNEY AGAIN INFORMATION:

CC REGISTRATION UNMBER: 0.30,764

CC REGISTRATION UNMBER: 0.36066

CC TELEPHONE: (202) 293-7060

CC TELEPHONE: (202) 293-7860

CC TELEPHONE: (202) 293-7860

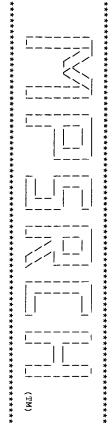
CC TELEPHONE: (202) 293-7860

CC TELEPHONE: 11.mear

CC TELEPHONE: (202) 293-7860

CC TELEPHONE: (202) 293-7860
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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Sat Apr 22 13:17:33 2000; MasPar time 44.93 Seconds 447.554 Million cell updates/sec

Tabular output not generated.

Description: Perfect Score:

Sequence: >US-09-422-999-18
(1-849) from US09422999.pep
6222
1 MYLMKRALIMTGFLIRRTHL.....VIDNQRTLSQMSHRLEPRRP 849

Scoring table: PAM 150 Gap 11

188963 segs, 23686106 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: a-geneseq36 1:geneseqp

Statistics: Mean 38.706; Variance 183.913; scale 0.210

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

1 3 3 3 4 4 4 4 4 7 7 1 1 1 1 1 1 1 1 1 1 1 1 1	Result No.
370 287 287 287 276 262 255 255 255 251 180 180 180 134 134 133 122 122 122 122 122 112 1116	Score
++++++5 +++++++5 +++++++++++++++++++++	Query Match I
1077 489 666 614 814 612 1297 1297 1297 1297 1297 1298 1316 609 728 932 758 528 528 528 528 528	Length I
	DB
R91597 R50991 R50990 R43578 R47048 R447048 R44638 R84638 R84638 R84638 W87994 W87994 W87994 W85040 W	Ħ
C3G protein. Peptide which modulate Mammalian son of seven mSOS2 protein. Peptide which modulate Mammalian son of seven mSOS1 protein. Peptide which modulate Peptide which modulate Peptide which modulate Peptide which protein a laternatively splica A human MCG7 protein. PKG-green fluorescent protein A pumpar MCG7 protein protescent fluorescent protein PKG-green fluorescent protein Seven Peptide Phytosacterium bovis la M. tuberculosis RNA po Virilence-associated s Mycobacterium bovis vi Sorting nexin 2. Rat GMEB-2 protein seg Rat GMEB-2 protein seg	Description
1.53e-19 9.88e-13 9.88e-13 9.88e-13 9.81e-11 1.00e-10 3.02e-10 3.63e-10 3.63e-10 3.63e-10 5.94e-06 2.29e-04 4.81e-01 5.64e-01 3.17e+00	Pred. No.

RESULT

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96 96	96 96	96 96	100	98	102	102	102	97	99	99	102	97	98	104	104	103	112
1.5	1.5	1.5	1.6	1.6	1.6	1.6	1.6	1.6	1.6	1.6	1.6	1.6	1.6	1.7	1.7	1.7	1.8
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W81839 W84560	R68838 R57283	W94458 W94459	W81512	W53485	W16326	W10653	W31504	R30477	W97809	R77249	W79140	W43421	R26181	W23969	W01113	W55710	W55252
Human LFA-1 alpha chai Polyprotein encoded by	Plasmodium falciparum Bovine enterokinase.	Human neurofibromatosi Human neurofibromatosi	Drosophila fat facets	Murine factor VIII.	Nematocidal toxin 167P	Bacillus thuringiensis	Nematode toxin 167P pr	Human leukocyteHGF.	Human GTPase regulator	Babesia merozoite p58.	Plant acetolactate syn	Rat syntaxin 3 protein	TSG-14.	Connexin protein Cx43.	RNA polymerase primary	ORF	H. pylori ORF 05ep1171
1.49e+02 1.49e+02	1.49e+02 1.49e+02	1.49e+02 1.49e+02	8.47e+01	1.13e+02	6.35e+01	6.35e+01	6.35e+01	1.30e+02	9.77e+01	9.77e+01	6.35e+01	1.30e+02	1.13e+02	4.75e+01	4.75e+01	5.49e+01	1.45e+01

ALIGNMENTS

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Best Local S
Matches 4
                                                                                         New peptide(s) modulating GDP exchange in complexes - with ras protein and derived antibodles, nucleic acid etc. esp. for diagnosis and treatment of cancer Claim 2; Page 23-24; 46pp; French.

The peptide antagonises the interaction of GDP-exchange factor (With the p21-GDP complex and thereby regulates the activity of 1 gene products. It can also be used to identify other compounds which can modulate GDP exchange. The coding sequence can be use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            diagnosis and treatment of cancer Claim 2; Page 25-26; 46pp; French.
The peptide antagonises the interaction of GDP-exchange factor (GRF with the p21-GDP complex and thereby regulates the activity of ras gene products. It can also be used to identify other compounds which can modulate GDP exchange. The coding sequence can be used to produce antisense products which can inhibit oncogene expression and for use in diagnosis e.g. detecting (over)expression of GRF for
                                                                                                                                                                                                                                                                                                                                        (RHON ) RHONE POULENC RORER Schweighoffer F, Tocque B; WPI; 93-351724/44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Peptide which modulates GDP; exchange; GRF; GDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (RHON) RHONE POULENC RORER Schweighoffer F, Tocque B; WPI; 93-351724/44.
                                                to produce antisense products and for use in diagnosis e.g.
                                                                                                                                                                                                                                                                                                                   N-PSDB; Q51233.
                                                                                                                                                                                                                                                                                                                                                                                                                  28-OCT-1993.
19-APR-1993; F00382.
21-APR-1992; FR-004827
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    detection; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R50990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R50990 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New peptide(s) modulating GDP exchange i protein and derived antibodies, nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; Q51233.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GDP; exchange; GRF; GDP exchange detection; cancer; ras; oncogene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens.
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R50991;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             exchange; GRF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KHFNDISNLIASEIIRNEDINARVSAIEKWVAVADICRCLHNYNAVLEITSSMNRSAIFR 359
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25.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GDP exchange factor; antisense; diagnosis;
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                                                   e.g. detecting
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  287; DB 1;
No. 9.88e-13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             in complexes acid etc. es
                                                inhibit oncogene expression (over)expression of GRF for
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Best Local
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New peptide(s) modulating GDP exchange in complexes - with ras protein and derived antibodies, nucleic acid etc. esp. for diagnosis and treatment of cancer Claim 2; Page 20-22; 46pp; French.

The peptide antagonises the interaction of GDP-exchange factor with the p21-GDP complex and thereby regulates the activity of gene products. It can also be used to identify other compounds which can modulate GDP exchange. The coding sequence can be used to the coding sequence ca
                                               Peptide which modulates GDP; exchange; GRF; GDP detection; cancer; ras;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (RHON ) RHONE POULENC RORER Schweighoffer F, Tocque B; WPI; 93-351724/44.
                                                                                                                     R43580;
11-MAY-1994
  Homo sapiens.
W09321314-A.
                                                                                                                                                                     R43580 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
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21-APR-1992; FR-0048
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       detection; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GDP; exchange;
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Local Similarity 25.6%;
nes 40; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    produce antisense products which can difor use in diagnosis e.g. detecting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                RRFNEIQFWVVTEICLCSQLSKRVQLLKKFIKIAAHCKEYKNLNSFFAIVMGLSNIAVSR 715
                                                                                                                                                                                                                                                                                                LALTWEKLPSKFKKFYAEFESLMDPSRNHRAYRLTVAKLEPPLIPFMPLLIKDMTFTHEG
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Pred. No. 9.1
49; Mismatcl
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Pred. No. 9.88e-13;
49; Mismatches 66
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                                                                        factor;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1;
.88e-13;
                                                                                               the p21-GDP
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19-APR-1993;
21-APR-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    diagnosis and treatment of cancer Claim 2; Page 32-34; 46pp; French.
The peptide antagonises the interaction of GDP-exchange factor (GRF with the p21-GDP complex and thereby regulates the activity of ras gene products. It can also be used to identify other compounds which can modulate GDP exchange. The coding sequence can be used to produce antisense products which can inhibit oncogene expression and for use in diagnosis e.g. detecting (over)expression of GRF for the contract of the canonic of th
                                                                                                                                                                    The mammalian son of sevenless gene has been found to have homology with various guanine exchange factors, suggesting a possible role in protein tyrosine kinase pathways via the Ras proteins. Mutations in the genes and consequently their products may result in specific defects or tumour formation. Antagonists to the protein/gene may used to treat conditions arising from mutations.
                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA encoding mammalian son of seven-less gene and proteins encoded by it - regulates tyrosine kinase signalling pathway ras proteins, may be used for diagnosis and therapy of genet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (FLOR-) FLOREY INST
Bowtell DDL;
WPI; 93-272883/34.
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17-FEB-1993; AU0068.
17-FEB-1992; AU-000921
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R47048
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Sequence 652 AA;
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Schweighoffer F, Tocque
WPI; 93-351724/44.
                                                                                                                                                                                                                                                                                                                                                                                                                     ras proteins, may defects
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26-MAY-1994 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New peptide(s) modulating GDP exchange in complexes - with protein and derived antibodies, nucleic acid etc. esp. for
                                                                                                                                                                                                                                                                                                                                                                                          Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; Q58624.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus.
W09316179-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        tyrosine kinase;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mammalian son
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          169
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y Match 4.3%;
Local Similarity 24.9%;
hes 57; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PLLIKDMTFTHEGNKTFI---D-NLVNFEKMRMIANTARTVRYYRSQPF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IVSAVNSVSYRLDHTFEALQERKRKIL-D-EA-VELSQDHFKKYLVKLKSINPPCVPFF 285
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GIYLTNILKTEEGNNDFLKKKGKDLINFSKRRKVAEITGEIQQYQNQPY
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                                                                                                                                                                                                                                                                                                                                                                                          6; Figure 2; 78pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    standard;
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                                                                                                                                         1297
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llarity 25.8%;
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que B;
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; Sos; guanine exchang
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Score 266; DB 1; L
Pred. No. 4.81e-11;
70; Mismatches 92;
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.60e-12;
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                                                                    Length 1297;
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Mouse mSOS2 (R84639) is a Ras guanine nucleotide releasing protein. The SH3 domains of Grb2 associate the the proline-rich domains of mSOS2 and mSOS1 (R84638). Synthetic peptides (R84640-48) based on these motifs can be used to screen for compounds that affect BCL-ABL mediated transformation. Such compounds have value in the treatment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Arlinghaus R, Gis WPI; 95-302931/40. N-PSDB; T05114.
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14-JAN-1994; 113494.
14-JAN-1994; CA-113494
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25-FEB-1996
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(TEXA ) UNIV TEXAS.
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894 GIYLTNILKTEEGNSDFLKRKGKDLINESKRRKVAEITGEIQQYQNQPY
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Similarity 24.9%;
57; Conservative
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,_apel= Proline-rich_motif

1164. 1176

/label= Proline-rich_motif

1178. 117
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/label= Proline-rich_motif
/label= Proline-r'
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70; M
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No. 1.00e-10;
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21-APR-1992; FR-004827.
(RHON ) RHONE POULENC RORE
Schweighoffer F, Tocque E
WPI; 93-351724/44.
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R43579;
R43579;
11-MAY-1994
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New peptide(s) modulating GDP exchange in complexes protein and derived antibodies, nucleic acid etc. es diagnosis and treatment of cancer Claim 2; Page 28-29; 46pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                              R47043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The peptide antagonises the interaction of GDP-exchange factor (GRF) with the p21-GDP complex and thereby regulates the activity of ras gene products. It can also be used to identify other compounds which can modulate GDP exchange. The coding sequence can be used to produce antisense products which can inhibit oncogene expression and for use in diagnosis e.g. detecting (over)expression of GRF for
                 DNA encoding mammalian son of seven-less gene and proteins encoded by it - regulates tyrosine kinase signalling pathway via ras proteins, may be used for diagnosis and therapy of genetic
                                                                                                             (FLOR-) FLOREY INST EXPERIMENTAL BOWtell DDL; WPI; 93-272883/34.
                                                                                                                                                                                                         19-AUG-1993.
17-FEB-1993; AU0068
                                                                                                                                                                                                                                                                                                         Son of sevenless gene; m
tyrosine kinase; tumour.
                                                                                                                                                                                                                                                                                                                                                                              R47043;
26-MAY-1994
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                                                                                           N-PSDB; Q48610.
                                                                                                                                                                                         17-FEB-1992; AU-000921
                                                                                                                                                                                                                                                                                                                                                          Mammalian
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58; Conse
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larity 25.48;
Conservative
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h modulates GDP exchange
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Pred. No. 3.02e-10;
65; Mismatches 97;
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                                                                            Detection of agents that modify BCR-ABL mediated transformation useful in treatment of leukaemia and other malignancies Disclosure; Page 54-59; 105pp; English.

Mouse mSOS1 (R84638) is a Ras guanine nucleotide releasing protein that combines with BCR-ABL and Grb2 (R84636) to activate the Ras pathway leading to morphological transformation. The SH3 domains of Grb2 associate the the proline-rich domains of mSOS1 and mSOS2 (R84639). Synthetic peptides (R84640-48) based on these motifs can be used to screen for compounds that affect BCL-ABL mediated transformation. Such compounds have value in the treatment of chronic, acute myelogenous or acute lymphocytic leukaemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LT 10
R84638
R84638;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 4; Figure 1; 78pp; English.
The mammalian son of sevenless gene has been found to have homology with various quanine exchange factors, suggesting a possible role in protein tyrosine kinase pathways via the Ras proteins. Mutations in the genes and consequently their products may result in specific defects or tumour formation. Antagonists to the protein/gene may be used to treat conditions arising from mutations.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  mSOS1 protein.
mSOS1; SOS1; Grb2; BCR-ABL; oncoprotein; leukaemia; Ras
                                                                  transformation. Such comports chronic, acute myelogenous sequence 1336 AA;
                                                                                                                                                                                                                                                                                                                                                                        CA2113494-A.
15-JUL-1995.
                                                                                                                                                                                                                                                                          Arlinghaus R, Gis
WPI; 95-302931/40.
                                                                                                                                                                                                                                                                                                    14-JAN-1994; 113494.
14-JAN-1994; CA-113494.
(MOUN ) MOUNT SINAL HOSPITAL CORP.
(TEXA ) UNIV TEXAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus.
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4.18;
Similarity 25.48;
58; Conservet
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1288. .1300
/label= Proline
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1210
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1178. .1
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25.48;
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                                                                                                                                                                                                                                                                                           Liu J, Pawson
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 Score 255; DB 1;
Pred. No. 3.63e-10;
64; Mismatches 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tyrosine kinase; transformation; Ras; guanine nucleotide releasing protein.
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Pred.
64; M
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No. 3.63e-10;
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05-SEP-1997; G02394.
08-APR-1997; GB-007132.
06-SEP-1996; GB-018600.
(CLIN-) CENT CLINICAL & BASIC RE
BYTJALSEN I, Fey SJ, Larsen P;
WPI: 98-207057/18.
Homo sapiens.

W09853061-A1.

26-NOV-1998.

22-MAY-1998; AU0380.

22-JAN-1998; AU-001460.

23-MAY-1997; AU-006972.
                                                                                                                                                                                MCG4 protein; gene guanine nucleotide heat shock-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  phase of the endometrium. The presence and quantities of these proteins can be detected using 2D gel electrophoresis comparison of cell lysates. The proteins can be used as biochemical markers to detect the phase of the endometrium and can be measured in body fluids, obviating the need for endometrial biopsies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Biochemical markers of human endometrium - useful for, diagnosis of hyperplasia and adenocarcinoma Disclosure; Page 19-20; 77pp; English. Proteins W54349-W54364 are examples of proteins produce endometrium during the hyperplasia, adenocarcinoma or the hyperplasia, adenocarcinoma or the hyperplasia.
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W54350;
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W87995 standard;
W87995;
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Local Similarity 31.7%;
                                                                                                                                                                                                                                                               alternatively
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                                                                                                                                                                                                                                                                                                                                          Protein;
                                                                                                                                                                             pliced human MCG7 protein.
regulatory function; heat shock protein;
exchange factor protein; MCG7 protein;
exchange factor protein; zinc finger protein;
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The presence and quantities of these pro
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26-NOV-1998,

22-MAY-1998,

22-MAY-1998,

23-MAY-1997,

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23-MAY-1997,
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The present sequence represents a MCG7 protein. The protein has gene regulatory functions, and has monology to a heat shock protein or heat shock-binding protein. The specification also describes MCG4, which is homologous to guanine nucleotide exchange factor protein, and MCG18, which is homologous to a zinc finger protein.

Detection of mutations in the MCG genes can be used to identify the propensity for various types of cancer, and to treat, arrest, or otherwise ameliorate, the effects of a cancer in an animal or bird.
New gene-expression regulatory genes, mcg4, mcg7, and mcg18 - encode a zinc finger protein, a GEF, and a heat shock or heat shock binding protein, useful to detect and treat cancer claim 5; Fig 13a; 80pp; English.

The present sequence represents a MCG7 protein. The protein has gene regulatory functions, and has homology to a heat shock protein or heat shock-binding protein. The specification also describes MCG4, which is homologous to guanine nucleotide exchange factor protein, and MCG18, which is homologous to a zinc finger protein. Detection of mutations in the MCG genes can be used to identify the propensity for various types of cancer, and to treat, arrest, or
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23-MAY-1997; AU-006974.
22-JAN-1998; AU-001458.
22-JAN-1998; AU-001459.
(COUN-) COUNCIL QUEENSLAND INST MEDICAL RES
Gartside M., Grimmond S, Hancock J, Hayward 1
                                                                                                                                                                                           WPI; 99-070146/06.
N-PSDB; X04552.
                                                                                                                                                                                                                                                                                                                                                                                                                                    cancer
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15-APR-1999
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22-JAN-1998; AU-001459.
22-JAN-1998; AU-001459.
(COUN-) COUNCIL QUEENSLAND INST MEDICAL RES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A human MCG7 protein.
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Similarity 26.4%;
38; Conservative
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AU-006973.
AU-006974.
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34; Mismatc
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                                                                                                                                                                                                                                                                                     per Determining effect on signalling pathways in live cells from redistribution of luminophores - specifically fusions of green fluorescent protein with a signalling component, and new apparatus, protein redistribution of luminophores - specifically fusions of green fluorescent protein with a signalling component, and new apparatus, protein respective for identifying toxins and potential therapeutic agents example 10; Pages 281-283; 326pp; English.

The present sequence represents a human PKG-green fluorescent protein (GFP) fusion protein. The fusion protein is used in an assay to examplify the invention. The specification describes how quantitative information about the influence of a molecule on a cellular response is obtained by recording the variation, caused by the molecule on mechanically intact living cells, in the spatially distributed light emitted from a luminophore present in the cells. The variation in light camission is processed to provide information that correlates spatial distribution to the degree of the molecule. The method is used to identify agents that (in)directly affect intracellular signalling, especially to screen for potential therapeutic agents or toxins, and to identify new drug targets.
                                                                                                                                                                                                     Query Match
Best Local S
Matches 3
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07-APR-1997; DK-000392.
(NOVO ) NOVO-NORDISK AS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           intracellular signalling;
Chimeric - Aequorea victo
Chimeric - Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; V71085
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kasper A, Petersen
Tullin S;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          606 FELMSSKDLAYQMTIYDWELFNCVHELELIYHTFGRHNFKKTTANLDLFLRRFNEIQFWV
                                                                                                   286
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299 E 299
                               344 D 344
                                                                                                                                     186 YEELLH-IKALSHLSTTVKRELAGVLIFESHAKGGTVLFNQGEEGTSWYIILKGSVNVVI 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2.9%;
Local Similarity 26.4%;
nes 38; Conservation
                                                                                                                                                       YMEFLKSVPTFQSLPEEILSKLADVLE-ETHYENGEYIIRQGARGDTFFIISKGTVNVTR 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98-594491/50.
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                                                                    --Y-GKG-V-VCTLHEGDDFGKLALVNDAPRAASIVLRED-NCHFLRVDKEDFNRILRDV
                                                                                                   EDSPSEDPVFLRTLGKGDWFGEKALQGEDVRTANVIAAEAVTC--LVIDRDSFKHLIGGL 343
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Similarity 30.6%;
37; Conservative
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                                                                                                                                                                                                                                                                            932 AA;
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                                                                                                                                                                                                     Score 134; DB 1; pred. No. 4.81e-01; 28; Mismatches 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Scudder K, Thastrup
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 180; DB 1;
Pred. No. 2.29e-04;
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Search completed: Sat Apr 22 13:18:22 2000 Job time: 49 secs.

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DR N-SDB; V7184.

DR N-SDB; V7184.

DR N-SDB; V7184.

PT redistribution of luminophores - specifically fusions of green redistribution of luminophores - specifically fusions of green process of present sequence represents and potential therapeutic agents process particularly for identifying toxins and potential therapeutic agents process particularly for identifying toxins and potential therapeutic agents process agreen fluorescent protein (GFP)-human CC processed sequence represents a green fluorescent protein (GFP)-human CC processed information. The influence of a molecule on a cellular response is contained by recording the variation, caused by the molecule, on the molecule processed to provide information that correlates spatial consistion is processed to provide information that correlates spatial consistion is processed to provide information that correlates spatial constitution to the degree of the molecule. The method is used to identify agents that (in)directly affect intracellular signalling, considered in the spatial therapeutic agents or toxins, and to consist the consist of the molecule.
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Best Local :
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07-APR-1997; DK-000392.
(NOVO ) NOVO-NORDISK AS.
Kasper A, Petersen Bjorn S
Tullin S;
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Human, PKG gene; fusion protein; g
intracellular signalling; chimera.
Chimeric Requorea victoria.
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Chimeric - Homo sapiens
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299 E
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                                      591 D
                                                                          245 --Y-GKG-V-VCTLHEGDDFGKLALVNDAPRAASIVLRED-NCHFLRVDKEDFNRILRDV
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Similarity 30.6%;
37; Conservation
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pred. No. 4.81e-01;
28; Mismatches 46
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in; green fluorescent protein; GFP;
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